



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 168291

TO: Jeffrey Parkin
Location: REM-3D39/3C18
Art Unit: 1648
Monday, August 01, 2005
Case Serial Number: 10/085944

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Parkin,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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160291

STIC-Biotech/ChemLib

From: Parkin, Jeffrey
Sent: Saturday, July 23, 2005 6:59 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search for U.S. Serial No. 10/085,944

Please search SEQ ID NOS.: 1 and 2 from the aforementioned application (U.S. Serial No. 10/085,944) v. all relevant databases. Place results on both paper and electronic format (i.e., disk, e-mail, etc.).

Thanks!

JSP
AU 1648
REM 3D39
2-0908

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 10:46:20 ; Search time 818 Seconds
(without alignments)
1658.614 Million cell updates/sec

Title: US-10-085-944-1
Perfect score: 28
Sequence: 1 cccattctcannatccctgctgttgg 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

- 1: gb_ba.*
- 2: gb_btg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	25	89.3	339	14	AY612201 Dengue vi
C 2	25	89.3	339	14	AY612202 Dengue vi
C 3	25	89.3	339	14	AY612203 Dengue vi
C 4	25	89.3	339	14	AY612204 Dengue vi
C 5	25	89.3	339	14	AY612205 Dengue vi
C 6	25	89.3	339	14	AY612207 Dengue vi
C 7	25	89.3	339	14	AY612208 Dengue vi
C 8	25	89.3	2319	14	S66064 structural
C 9	25	89.3	2325	14	AF469175 Dengue vi
C 10	25	89.3	2325	14	AF469176 Dengue vi
C 11	25	89.3	2357	6	AR232496 Sequence
C 12	25	89.3	2357	14	DEN2NGC
C 13	25	89.3	2552	14	AY152036S1
C 14	25	89.3	2552	14	AY152040S1
C 15	25	89.3	2552	14	AY152044S1
C 16	25	89.3	2552	14	AY152048S1
C 17	25	89.3	2552	14	AY152052S1
C 18	25	89.3	2552	14	AY152056S1
C 19	25	89.3	2552	14	AY152060S1

25	89.3	2552	14	AY152064S1	Dengue vi
25	89.3	2552	14	AY152068S1	Dengue vi
25	89.3	2552	14	AY152072S1	Dengue vi
25	89.3	2552	14	AY152076S1	Dengue vi
25	89.3	2552	14	AY152080S1	Dengue vi
25	89.3	2552	14	AY152084S1	Dengue vi
25	89.3	2552	14	AY152088S1	Dengue vi
25	89.3	2552	14	AY152092S1	Dengue vi
25	89.3	2552	14	AY152100S1	Dengue vi
25	89.3	2552	14	AY152104S1	Dengue vi
25	89.3	2552	14	AY152108S1	Dengue vi
25	89.3	2552	14	AY152112S1	Dengue vi
25	89.3	2552	14	AY152116S1	Dengue vi
25	89.3	2552	14	AY152120S1	Dengue vi
25	89.3	2552	14	AY152124S1	Dengue vi
25	89.3	2552	14	AY152128S1	Dengue vi
25	89.3	2552	14	AY152132S1	Dengue vi
25	89.3	2552	14	AY152136S1	Dengue vi
25	89.3	2552	14	AY152140S1	Dengue vi
25	89.3	2552	14	AY152144S1	Dengue vi
25	89.3	2552	14	AY152148S1	Dengue vi
25	89.3	2552	14	AY152152S1	Dengue vi
25	89.3	2552	14	AY152156S1	Dengue vi
25	89.3	2552	14	AY152160S1	Dengue vi
25	89.3	2552	14	AY152164S1	Dengue vi
25	89.3	2552	14	AY152168S1	Dengue vi
25	89.3	2552	14	AY152172S1	Dengue vi
25	89.3	2552	14	AY152176S1	Dengue vi
25	89.3	2552	14	AY152180S1	Dengue vi
25	89.3	2552	14	AY152184S1	Dengue vi
25	89.3	2552	14	AY152188S1	Dengue vi
25	89.3	2552	14	AY152192S1	Dengue vi
25	89.3	2552	14	AY152196S1	Dengue vi
25	89.3	2552	14	AY152200S1	Dengue vi
25	89.3	2552	14	AY152204S1	Dengue vi
25	89.3	2552	14	AY152208S1	Dengue vi
25	89.3	2552	14	AY152212S1	Dengue vi
25	89.3	2552	14	AY152216S1	Dengue vi
25	89.3	2552	14	AY152220S1	Dengue vi
25	89.3	2552	14	AY152224S1	Dengue vi
25	89.3	2552	14	AY152228S1	Dengue vi
25	89.3	2552	14	AY152232S1	Dengue vi
25	89.3	2552	14	AY152236S1	Dengue vi
25	89.3	2552	14	AY152240S1	Dengue vi
25	89.3	2552	14	AY152244S1	Dengue vi
25	89.3	2552	14	AY152248S1	Dengue vi
25	89.3	2552	14	AY152252S1	Dengue vi
25	89.3	2552	14	AY152256S1	Dengue vi
25	89.3	2552	14	AY152260S1	Dengue vi
25	89.3	2552	14	AY152264S1	Dengue vi
25	89.3	2552	14	AY152268S1	Dengue vi
25	89.3	2552	14	AY152272S1	Dengue vi
25	89.3	2552	14	AY152276S1	Dengue vi
25	89.3	2552	14	AY152280S1	Dengue vi
25	89.3	2552	14	AY152284S1	Dengue vi
25	89.3	2552	14	AY152288S1	Dengue vi
25	89.3	2552	14	AY152292S1	Dengue vi
25	89.3	2552	14	AY152296S1	Dengue vi
25	89.3	2552	14	AY152300S1	Dengue vi
25	89.3	2552	14	AY152304S1	Dengue vi
25	89.3	2552	14	AY152308S1	Dengue vi
25	89.3	2552	14	AY152312S1	Dengue vi
25	89.3	2552	14	AY152316S1	Dengue vi
25	89.3	2552	14	AY152320S1	Dengue vi
25	89.3	2552	14	AY152324S1	Dengue vi
25	89.3	2552	14	AY152328S1	Dengue vi
25	89.3	2552	14	AY152332S1	Dengue vi
25	89.3	2552	14	AY152336S1	Dengue vi
25	89.3	2552	14	AY152340S1	Dengue vi
25	89.3	2552	14	AY152344S1	Dengue vi
25	89.3	2552	14	AY152348S1	Dengue vi
25	89.3	2552	14	AY152352S1	Dengue vi
25	89.3	2552	14	AY152356S1	Dengue vi
25	89.3	2552	14	AY152360S1	Dengue vi
25	89.3	3381	14	DVU31949	Dengue viru
25	89.3	3381	14	DVU31950	Dengue viru
25	89.3	3381	14	DVU31951	Dengue viru
25	89.3	10597	14	DV1487271	Dengue vi

C 93	25	89.3	10618	14	AF326826	AF326826 Dengue vi	C 166	23.4	83.6	10648	6	AX224231	AX224231 Sequence
C 94	25	89.3	10618	14	AF326827	AF326827 Dengue vi	C 167	23.4	83.6	10648	6	AX224233	AX224233 Sequence
C 95	25	89.3	10648	14	DENSTRA	M14931 Dengue viru	C 168	23.4	83.6	10665	14	AF289029	AF289029 dengue vi
C 96	25	89.3	10649	14	AF326573	AF326573 Dengue vi	C 169	23.4	83.6	10674	14	AF100467	AF100467 Dengue vi
C 97	25	89.3	10649	14	AF326825	AF326825 Dengue vi	C 170	23.4	83.6	10674	14	AF100468	AF100468 Dengue vi
C 98	25	89.3	10649	14	AF375882	AF375882 Dengue vi	C 171	23.4	83.6	10684	14	AF100462	AF100462 Dengue vi
C 99	25	89.3	10682	14	AF100466	AF100466 Dengue vi	C 172	23.4	83.6	10722	14	AF489932	AF489932 Dengue V1
C 100	25	89.3	10685	14	AF100459	AF100459 Dengue vi	C 173	23.4	83.6	10723	14	AF022437	AF022437 Dengue vi
C 101	25	89.3	10685	14	AF100460	AF100460 Dengue vi	C 174	23.4	83.6	10723	14	AF022438	AF022438 Dengue vi
C 102	25	89.3	10685	14	AF100461	AF100461 Dengue vi	C 175	23.4	83.6	10723	14	AF022439	AF022439 Dengue vi
C 103	25	89.3	10685	14	AF100463	AF100463 Dengue vi	C 176	23.4	83.6	10723	14	AF119861	AF119861 Dengue vi
C 104	25	89.3	10685	14	AF100464	AF100464 Dengue vi	C 177	23.4	83.6	10723	14	M20558	Dengue viru
C 105	25	89.3	10717	6	AX224217	AX224217 Sequence	C 178	23.4	83.6	10723	14	AF593218	AF593218 Dengue vi
C 106	25	89.3	10723	6	AX224219	AX224219 Sequence	C 179	21.8	77.9	350	14	AF593218	AF593218 Dengue vi
C 107	25	89.3	10723	6	AX224221	AX224221 Sequence	C 180	21.8	77.9	350	14	AF593219	AF593219 Dengue vi
C 108	25	89.3	10723	6	AX224223	AX224223 Sequence	C 181	21.8	77.9	350	14	AF593221	AF593221 Dengue vi
C 109	25	89.3	10723	6	AX224235	AX224235 Sequence	C 182	21.8	77.9	350	14	AF593222	AF593222 Dengue vi
C 110	25	89.3	10723	14	AF022435	AF022435 Dengue vi	C 183	21.8	77.9	350	14	AF593223	AF593223 Dengue vi
C 111	25	89.3	10723	14	AF022436	AF022436 Dengue vi	C 184	21.8	77.9	350	14	AF593224	AF593224 Dengue vi
C 112	25	89.3	10723	14	AF022440	AF022440 Dengue vi	C 185	21.8	77.9	350	14	AF593225	AF593225 Dengue vi
C 113	25	89.3	10723	14	AF022441	AF022441 Dengue vi	C 186	21.8	77.9	350	14	AF593226	AF593226 Dengue vi
C 114	25	89.3	10723	14	AF159678	AF159678 Dengue vi	C 187	21.8	77.9	350	14	AF593227	AF593227 Dengue vi
C 115	25	89.3	10723	14	AF159679	AF159679 Dengue vi	C 188	21.8	77.9	350	14	AF593228	AF593228 Dengue vi
C 116	25	89.3	10723	14	AF159680	AF159680 Dengue vi	C 189	21.8	77.9	366	14	AF047401	AF047401 Dengue vi
C 117	25	89.3	10723	14	AF159681	AF159681 Dengue vi	C 190	21.8	77.9	367	14	AF047393	AF047393 Dengue vi
C 118	25	89.3	10723	14	AF159682	AF159682 Dengue vi	C 191	21.8	77.9	376	14	AF047395	AF047395 Dengue vi
C 119	25	89.3	10723	14	AF159683	AF159683 Dengue vi	C 192	21.8	77.9	400	14	AF324614	AF324614 Dengue vi
C 120	25	89.3	10723	14	AF159684	AF159684 Dengue vi	C 193	21.8	77.9	400	14	AF324615	AF324615 Dengue vi
C 121	25	89.3	10723	14	AF159685	AF159685 Dengue vi	C 194	21.8	77.9	400	14	AF324616	AF324616 Dengue vi
C 122	25	89.3	10723	14	AF159686	AF159686 Dengue vi	C 195	21.8	77.9	400	14	AF324617	AF324617 Dengue vi
C 123	25	89.3	10723	14	AF159687	AF159687 Dengue vi	C 196	21.8	77.9	400	14	AF324618	AF324618 Dengue vi
C 124	25	89.3	10723	14	AF159688	AF159688 Dengue vi	C 197	21.8	77.9	400	14	AF324619	AF324619 Dengue vi
C 125	25	89.3	10723	14	AF204177	AF204177 Dengue vi	C 198	21.8	77.9	400	14	AF324620	AF324620 Dengue vi
C 126	25	89.3	10723	14	AF204178	AF204178 Dengue vi	C 199	21.8	77.9	400	14	AF324621	AF324621 Dengue vi
C 127	25	89.3	10723	14	DENCCGA	M29095 Dengue viru	C 200	21.8	77.9	400	14	AF324622	AF324622 Dengue vi
C 128	25	89.3	10723	14	DENCMEMSA	M84728 Dengue viru	C 201	21.8	77.9	400	14	AF324623	AF324623 Dengue vi
C 129	25	89.3	10723	14	DENCMEMSB	M84727 Dengue viru	C 202	21.8	77.9	400	14	AF324624	AF324624 Dengue vi
C 130	25	89.3	10723	14	U87411	U87411 Dengue viru	C 203	21.8	77.9	403	14	AF047398	AF047398 Dengue vi
C 131	25	89.3	10723	14	U87412	U87412 Dengue viru	C 204	21.8	77.9	405	14	AF047396	AF047396 Dengue vi
C 132	25	89.3	10724	14	AF022434	AF022434 Dengue vi	C 205	21.8	77.9	406	14	AF047394	AF047394 Dengue vi
C 133	25	89.3	10724	14	AF038402	AF038402 Dengue vi	C 206	21.8	77.9	406	14	AF047397	AF047397 Dengue vi
C 134	25	89.3	10724	14	AF038403	AF038403 Dengue vi	C 207	21.8	77.9	406	14	AF047400	AF047400 Dengue vi
C 135	25	89.3	10756	6	AX224225	AX224225 Sequence	C 208	21.8	77.9	406	14	AF047402	AF047402 Dengue vi
C 136	25	89.3	15237	12	AY243469	AY243469 Chimeric	C 209	21.8	77.9	454	14	AF177541	AF177541 Dengue vi
C 137	25	89.3	15239	12	AY243467	AY243467 Chimeric	C 210	21.8	77.9	454	14	AF706095	AF706095 Dengue vi
C 138	25	89.3	15239	12	AY376438	AY376438 Dengue vi	C 211	21.8	77.9	840	14	AF360860	AF360860 Dengue vi
C 139	25	89.3	15256	12	AY656168	AY656168 Chimeric	C 212	21.8	77.9	840	14	AF360861	AF360861 Dengue vi
C 140	25	89.3	15268	12	AY243468	AY243468 Chimeric	C 213	21.8	77.9	2325	14	AF509530	AF509530 Dengue vi
C 141	25	89.3	15270	12	AY243466	AY243466 Chimeric	C 214	21.8	77.9	2474	14	DENTAH	D00502 Dengue viru
C 142	25	89.3	15270	12	AY648301	AY648301 Dengue vi	C 215	21.8	77.9	3381	6	AR122077	AR122077 Sequence
C 143	25	89.3	15287	12	AY656167	AY656167 Chimeric	C 216	21.8	77.9	3381	6	AR122078	AR122078 Sequence
C 144	23.4	83.6	339	14	AY612206	AY612206 Dengue vi	C 217	21.8	77.9	3381	6	AR135737	AR135737 Sequence
C 145	23.4	83.6	342	14	FLD3CPM1	X51708 Dengue-2 vi	C 218	21.8	77.9	3381	6	AR135738	AR135738 Sequence
C 146	23.4	83.6	342	14	FLD3CPM2	X51709 Dengue-2 vi	C 219	21.8	77.9	3381	6	AR559088	AR559088 Sequence
C 147	23.4	83.6	342	14	FLD3CPM3	X51710 Dengue-2 vi	C 220	21.8	77.9	3381	6	BD073455	BD073455 Recombina
C 148	23.4	83.6	351	14	AY079176	AY079176 Dengue vi	C 221	21.8	77.9	3381	14	DVU88237	DVU88237 Dengue viru
C 149	23.4	83.6	405	14	AF047399	AF047399 Dengue vi	C 222	21.8	77.9	10674	14	AF100465	AF100465 Dengue vi
C 150	23.4	83.6	454	14	AF177542	AF177542 Dengue vi	C 223	21.8	77.9	10674	14	AF100469	AF100469 Dengue vi
C 151	23.4	83.6	454	14	AY706094	AY706094 Dengue vi	C 224	21.8	77.9	10703	14	DENRCG	M19397 Dengue viru
C 152	23.4	83.6	475	14	DEN3CPMP	274048 Dengue viru	C 225	21.8	77.9	10722	14	AF208496	AF208496 Dengue vi
C 153	23.4	83.6	840	14	AF360862	AF360862 Dengue vi	C 226	21.8	77.9	10723	14	AB122020	AB122020 Dengue vi
C 154	23.4	83.6	840	14	AF360863	AF360863 Dengue vi	C 227	21.8	77.9	10723	14	AB122021	AB122021 Dengue vi
C 155	23.4	83.6	2325	14	AY044442	AY044442 Dengue vi	C 228	21.8	77.9	10723	14	AB122022	AB122022 Dengue vi
C 156	23.4	83.6	2469	14	DENTAMA	M15075 Dengue viru	C 229	21.8	77.9	10723	14	AB189122	AB189122 Dengue vi
C 157	23.4	83.6	2552	14	AY152096S1	AY152096 Dengue vi	C 230	21.8	77.9	10723	14	AB189123	AB189123 Dengue vi
C 158	23.4	83.6	2552	14	AY152140S1	AY152140 Dengue vi	C 231	21.8	77.9	10723	14	AB189124	AB189124 Dengue vi
C 159	23.4	83.6	2552	14	AY152256S1	AY152256 Dengue vi	C 232	21.8	77.9	10723	14	AF276619	AF276619 Dengue vi
C 160	23.4	83.6	2552	14	AY152260S1	AY152260 Dengue vi	C 233	21.8	77.9	10723	14	AF359579	AF359579 Dengue vi
C 161	23.4	83.6	2552	14	AY152264S1	AY152264 Dengue vi	C 234	21.8	77.9	10723	14	AY037116	AY037116 Dengue vi
C 162	23.4	83.6	2552	14	AY152268S1	AY152268 Dengue vi	C 235	20.2	72.1	342	14	DEN2CPG	X65239 Dengue-2 vi
C 163	23.4	83.6	3381	14	DVU31952	U31952 Dengue viru	C 236	20.2	72.1	342	14	DV1CAPSID	X70952 Dengue viru
C 164	23.4	83.6	3381	14	DVU89517	U89517 Dengue viru	C 237	20.2	72.1	364	14	AY584591	AY584591 Dengue vi
C 165	23.4	83.6	3381	14	DVU89518	U89518 Dengue viru	C 238	20.2	72.1	364	14	AY584592	AY584592 Dengue vi

C 239	20.2	72.1	364	14	AY584593	AY584593 Dengue vi	C 312	19.2	68.6	2887	14	AY277654	AY277654 Dengue vi
C 240	20.2	72.1	364	14	AY584594	AY584594 Dengue vi	C 313	19.2	68.6	2887	14	AY277655	AY277655 Dengue vi
C 241	20.2	72.1	364	14	AY612195	AY612195 Dengue vi	C 314	19.2	68.6	2887	14	AY277656	AY277656 Dengue vi
C 242	20.2	72.1	364	14	AY612196	AY612196 Dengue vi	C 315	19.2	68.6	2887	14	AY277657	AY277657 Dengue vi
C 243	20.2	72.1	364	14	AY612198	AY612198 Dengue vi	C 316	19.2	68.6	2887	14	AY277658	AY277658 Dengue vi
C 244	20.2	72.1	364	14	AY612198	AY612198 Dengue vi	C 317	19.2	68.6	2887	14	AY277659	AY277659 Dengue vi
C 245	20.2	72.1	426	14	AY612200	AY612200 Dengue vi	C 318	19.2	68.6	2887	14	AY277660	AY277660 Dengue vi
C 246	20.2	72.1	436	14	AY638028	AY638028 Dengue vi	C 319	19.2	68.6	2887	14	AY277661	AY277661 Dengue vi
C 247	20.2	72.1	436	14	AY638023	AY638023 Dengue vi	C 320	19.2	68.6	2887	14	AY277662	AY277662 Dengue vi
C 248	20.2	72.1	483	14	AY638031	AY638031 Dengue vi	C 321	19.2	68.6	2887	14	AY277663	AY277663 Dengue vi
C 249	20.2	72.1	491	14	AY638030	AY638030 Dengue vi	C 322	19.2	68.6	10721	14	AF298807	AF298807 Dengue vi
C 250	20.2	72.1	493	14	AY638024	AY638024 Dengue vi	C 323	19.2	68.6	10735	14	AB074761	AB074761 Dengue vi
C 251	20.2	72.1	497	14	AY638027	AY638027 Dengue vi	C 324	19.2	68.6	10735	14	AF226685	AF226685 Dengue vi
C 252	20.2	72.1	501	14	AY638025	AY638025 Dengue vi	C 325	19.2	68.6	10735	14	AF226686	AF226686 Dengue vi
C 253	20.2	72.1	502	14	AY638026	AY638026 Dengue vi	C 326	19.2	68.6	10735	14	AF226687	AF226687 Dengue vi
C 254	20.2	72.1	506	14	DENICMP	774047 Dengue vi	C 327	19.2	68.6	10735	14	AF311956	AF311956 Dengue vi
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C 262	20.2	72.1	10705	14	DENT1SEQ	M87512 Dengue vi	C 335	19.2	68.6	10735	14	AF514889	AF514889 Dengue vi
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C 268	20.2	72.1	10723	6	AX224215	AX224215 Sequence	C 341	19.2	68.6	115431	9	AC010880	AC010880 Homo sapi
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C 270	20.2	72.1	10735	6	AX224209	AX224209 Sequence	C 343	19.2	68.6	146078	9	AC091874	AC091874 Homo sapi
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C 293	19.4	69.3	329457	2	AC103339	AC103339 Rattus no	C 366	18.8	67.1	43248	9	EX011932	EX011932 Human DNA
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C 306	19.2	68.6	364	14	AY593217	AY593217 Dengue vi	C 379	18.8	67.1	300029	8	AE017105	AE017105 Oryza sat
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C 309	19.2	68.6	2474	14	DENCCV	D00501 Dengue vi	C 382	18.6	66.4	290	14	AY079175	AY079175 Dengue vi
C 310	19.2	68.6	2887	14	AY277652	AY277652 Dengue vi	C 383	18.6	66.4	318	14	AF495889	AF495889 Dengue vi
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Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 79 CCCATCTCTTCATATCCCTGCTGTGG 52

RESULT 5
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LOCUS      339 bp      RNA      linear      VRL 06-OCT-2004
DEFINITION Dengue virus type 2 isolate 91/91/thailand polyprotein gene,
partial cds.
ACCESSION  AY612205
VERSION     AY612205.1  GI:53680724
KEYWORDS   .
SOURCE      Dengue virus type 2
ORGANISM    Dengue virus type 2
REFERENCE   1 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Dengue virus evolution in India and Thailand
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Direct Submission
JOURNAL     Submitted (29-APR-2004) Microbiology, All India Institute of
Medical Sciences, Ansari Nagar, New Delhi 110 029, India
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Db 79 CCCATCTCTTCATATCCCTGCTGTGG 52

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DEFINITION Dengue virus type 2 isolate T627/thailand polyprotein gene, partial
cds.
ACCESSION  AY612207
VERSION     AY612207.1  GI:53680728
KEYWORDS   .
SOURCE      Dengue virus type 2
ORGANISM    Dengue virus type 2
REFERENCE   1 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Dengue virus evolution in India and Thailand
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Direct Submission
JOURNAL     Submitted (29-APR-2004) Microbiology, All India Institute of
Medical Sciences, Ansari Nagar, New Delhi 110 029, India
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Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 79 CCCATCTCTTCATATCCCTGCTGTGG 52

RESULT 7
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LOCUS      339 bp      RNA      linear      VRL 06-OCT-2004
DEFINITION Dengue virus type 2 isolate T7/thailand polyprotein gene, partial
cds.
ACCESSION  AY612208
VERSION     AY612208.1  GI:53680730
KEYWORDS   .
SOURCE      Dengue virus type 2
ORGANISM    Dengue virus type 2
REFERENCE   1 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Dengue virus evolution in India and Thailand
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Direct Submission
JOURNAL     Submitted (29-APR-2004) Microbiology, All India Institute of
Medical Sciences, Ansari Nagar, New Delhi 110 029, India
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Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 79 CCCATCTCTTCAGTATCCCTGCTGTGG 52
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Query Match      89.3%; Score 25; DB 14; Length 339;
Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCTTCANNATCCCTGCTGTTGG 28
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Db 79 CCATCTCTTCATATCCCTGCTGTTGG 52

RESULT 8
S66064/c
LOCUS      2319 bp DNA linear VRL 04-DEC-1993
DEFINITION structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
2319 nt].
ACCESSION S66064.1 GI:432575
VERSION   1
KEYWORDS  Dengue virus type 4
SOURCE    Dengue virus type 4
ORGANISM  Dengue virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2319)
AUTHORS   Kawano,H., Rostapshov,V., Rosen,L. and Lai,C.J.
TITLE     Genetic determinants of dengue type 4 virus neurovirulence for mice
JOURNAL   J. Virol. 67 (11), 6567-6575 (1993)
MEDLINE   94016840
PUBMED    8411360
REMARK    GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138430] from the original journal article.

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Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 205 CCATCTCTTCAGATCCCTGCTGTTGG 178

RESULT 9
AF469175/c
LOCUS      2325 bp RNA linear VRL 20-FEB-2002
DEFINITION Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
ACCESSION AF469175
VERSION   1
KEYWORDS  Dengue virus type 2
SOURCE    Dengue virus type 2
ORGANISM  Dengue virus type 2
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2325)
AUTHORS   Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE     Structural genes of dengue virus type 2 strain GD24/93 isolate from
            Nanhai, Guangdong, China
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 2325)
AUTHORS   Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE     Direct Submission
JOURNAL   Submitted (16-JAN-2002) Department of Virology, The Military
            Medical Institute of Guangzhou Military District, Dong Guanzhuang
            Road 91, Guangzhou, Guangdong 5105407, China

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Query Match      89.3%; Score 25; DB 14; Length 2325;
Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 208 CCATCTCTTCATATCCCTGCTGTTGG 181
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ORIGIN

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RESULT 10
AF469176/c      2325 bp      RNA      linear      VRL 20-FEB-2002
LOCUS
DEFINITION      Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
ACCESSION       AF469176
VERSION         AF469176.1  GI:18766556
KEYWORDS
SOURCE
ORGANISM        Dengue virus type 2
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                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
AUTHORS         Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
                Zhao,W.Z.
TITLE           Structural genes of dengue virus type 2 strain GD24/93 isolate from
                Nanhai, Guangdong, China
JOURNAL
REFERENCE
2 (bases 1 to 2325)
AUTHORS         Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
                Zhao,W.Z.
TITLE           Direct Submission
JOURNAL
SUBMITTED (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
LOCATION/Qualifiers
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TRTETMSSEGAKHQRITWILRHFGFTIMAAIAYTTGTTGFORALIFILLTAVA
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IVTCAMTCKNMGKIVQENLEIYIWTTPHSGEHAIGNDTGKGKEIKVTPQSSV
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Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 11
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LOCUS
DEFINITION      Sequence 1 from patent US 6455509.
ACCESSION       AR232496
VERSION         AR232496.1  GI:27274633
KEYWORDS
SOURCE
ORGANISM        Unknown.
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                Unclassified.

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REFERENCE
AUTHORS         Kocheil,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
                Hayes,C.G.
TITLE           Dengue nucleic acid vaccines that induce neutralizing antibodies
JOURNAL
PATENT         US 6455509-A 1 24-SEP-2002;
LOCATION/Qualifiers
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LOCUS
DEFINITION      Dengue virus type 2 gene for polyprotein, partial cds, strain:New
                Guinea C.
ACCESSION       D00346
VERSION         D00346.1  GI:221230
KEYWORDS
SOURCE
ORGANISM        Dengue virus type 2
                Dengue virus type 2
                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2357)
AUTHORS         Gruenberg,A., Woo,W.S., Biedrzycka,A. and Wright,P.J.
TITLE           Partial nucleotide sequence and deduced amino acid sequence of the
                structural proteins of dengue virus type 2, New Guinea C and
                PUO-218 strains
JOURNAL         J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
MEDLINE
PUBMED         88258474
3385407
COMMENT         Nucleotide 1 in the NC sequence corresponds to nucleotide 77
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Query Match 89.3%; Score 25; DB 14; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 228 CCATCTCTTCAGATATCCCTGCTGTGG 201

RESULT 13
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LOCUS Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION AY152036
VERSION AY152036.1 GI:28170806
KEYWORDS 1 of 4
SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
ORGANISM Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 205 CCATCTCTTCAGATATCCCTGCTGTGG 178

RESULT 14
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LOCUS Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION AY152040
VERSION AY152040.1 GI:28170815
KEYWORDS 1 of 4
SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
ORGANISM Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCANTCANNATCCCTGCTGTGG 28
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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTTCAGAAATCCCTGCTGTGG 178
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RESULT 22
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DEFINITION Dengue virus type 4 D4.46_1998 polyprotein precursor, gene, partial
cds.
ACCESSION AY152072
VERSION AY152072.1 GI:28170887
KEYWORDS
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTTCAGAAATCCCTGCTGTGG 178
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RESULT 22
AY152072S1/c 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.46_1998 polyprotein precursor, gene, partial
cds.
ACCESSION AY152072
VERSION AY152072.1 GI:28170887
KEYWORDS
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
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Db 205 CCCATCTTCAGAAATCCCTGCTGTGG 178
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RESULT 22
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LOCUS
DEFINITION Dengue virus type 4 D4.48_1998 polyprotein precursor, gene, partial
cds.
ACCESSION AY152076
VERSION AY152076.1 GI:28170896
KEYWORDS
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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RESULT 26
AY152088S1/c
LOCUS      AY152088S1      2552 bp      RNA      linear      VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.44_1998 polyprotein precursor, gene, partial cds.
ACCESSION  AY152088
VERSION     AY152088.1  GI:28170923
KEYWORDS
SEGMENT
SOURCE
ORGANISM
REFERENCE
1 of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 205 CCCATCTCTTCAGAATCCCTGCTGTTGG 178
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DEFINITION Dengue virus type 4 D4.113_1995VQ polyprotein precursor, gene,
partial cds.
ACCESSION  AY152092
VERSION     AY152092.1  GI:28170932
KEYWORDS
SEGMENT
SOURCE
ORGANISM
REFERENCE
1 of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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Query Match      89.3%; Score 25; DB 14; Length 2552;
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DEFINITION Dengue virus type 4 D4.112_1995MQ polyprotein precursor, gene,
partial cds.
ACCESSION  AY152100
VERSION     AY152100.1  GI:28170950
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SEGMENT
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1 of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
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2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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CDS 1. .>2552 /organism="Dengue virus type 4" /mol_type="genomic RNA" /isolate="D4.112.1995MQ" /db_xref="taxon:11070" /country="Martinique" /note="acronym: DEN-4" 1. .>2552 /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="AAN38387.1" /db_xref="GI:28170957" /translation="MNORKKVVPPFNMLKRRNRVSTPQGLVKRFSTGLFSGKGPLR MVLAFITFLRVLSIPTTAGILKRWGLKQKRAIKILIGPRKEIGRMNLINLGRKRSTI TLLCLIPFWAFHLSTEDGEPLMIVAKHERGRPLLPKTTGINKKTLIANDLGEMCED TVYKCLIPWAFHLSTEDGEPLMIVAKHERGRPLLPKTTGINKKTLIANDLGEMCED RAETWMSSEGLAWKQVSEWILNPGFALLAGFMAYMIGQGTQRTVFFVLMMLVAP SYGMRCVGVGNRDFVEVSGGAWDLVLEHGGCVTTMAQCKPLDPLFTKTAKEVAL LRTYCIASISNITTATRCPTQGEPLKEBQDOQYICRRDVRDVGWNGGGLFGKGV VTCAPKSCSGKITGNLVOIENLEYTVVTVHNGDTHAVNGDTHSHGVTATITPRSPV EVKLPDYBELTDCPEPSGIDENEMILMKKKKTLVHKQFMDLPLPWTAGADTSEV HWYKERMVTFKVPKARQDVTVLGSEGMHSAALAGATEVDSGDGNHMFAGHLKCKV RMEKLRIGMSYTCSCGFSIDKEMASTQHTTVKVKYEGAGAPCKVPIEIRDVNKE KVGVRVISTPLAENTSVNIELEPPGDSYIVIGVNSALTLMHFRKSSIGKMPF STYKGAERMAILGETAWDFSGVGLFTSLGKAVHGVFSGVYTTMFGVSGWIRILIGF LVLWIGTNSRNTSMATCIAGVGITLPLGFTVQADMGCVCVWSGRELKCSGIFVVDN VHTWTQYKQFESPARLASAILNAHKDGVCGITRSTRLNVMVMKQITNELN"

ORIGIN Query Match 89.3%; Score 25; DB 14; Length 2552; Best Local Similarity 89.3%; Pred. No. 0.97; Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28 ||||| ||||| ||||| ||||| ||||| Db 205 CCCATCTCTCAGAATCCCTGCTGTGG 178

RESULT 29 AY152104S1/c AY152104S1 2552 bp RNA linear VRL 29-SEP-2003 LOCUS Dengue virus type 4 D4.108_1996CR polyprotein precursor, gene, partial cds. DEFINITION ACCESSION AY152104.1 GI:28170959 VERSION 1 of 4 KEYWORDS Dengue virus type 4 (DEN-4) ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group. 1 (bases 1 to 2552) Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003) 12832629

REFERENCE 2 (bases 1 to 2552) Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico 12832629

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Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES source 1. .2552 /organism="Dengue virus type 4" /mol_type="genomic RNA" /isolate="D4.108_1996CR" /db_xref="taxon:11070" /country="Costa Rica" /note="acronym: DEN-4" 1. .>2552 /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="AAN38391.1" /db_xref="GI:28170966" /translation="MNORKKVVPPFNMLKRRNRVSTPQGLVKRFSTGLFSGKGPLR MVLAFITFLRVLSIPTTAGILKRWGLKQKRAIKILIGPRKEIGRMNLINLGRKRSTI TLLCLIPFWAFHLSTEDGEPLMIVAKHERGRPLLPKTTGINKKTLIANDLGEMCED TVYKCLIPWAFHLSTEDGEPLMIVAKHERGRPLLPKTTGINKKTLIANDLGEMCED RAETWMSSEGLAWKQVSEWILNPGFALLAGFMAYMIGQGTQRTVFFVLMMLVAP SYGMRCVGVGNRDFVEVSGGAWDLVLEHGGCVTTMAQCKPLDPLFTKTAKEVAL LRTYCIASISNITTATRCPTQGEPLKEBQDOQYICRRDVRDVGWNGGGLFGKGV VTCAPKSCSGKITGNLVOIENLEYTVVTVHNGDTHAVNGDTHSHGVTATITPRSPV EVKLPDYBELTDCPEPSGIDENEMILMKKKKTLVHKQFMDLPLPWTAGADTSEV HWYKERMVTFKVPKARQDVTVLGSEGMHSAALAGATEVDSGDGNHMFAGHLKCKV RMEKLRIGMSYTCSCGFSIDKEMASTQHTTVKVKYEGAGAPCKVPIEIRDVNKE KVGVRVISTPLAENTSVNIELEPPGDSYIVIGVNSALTLMHFRKSSIGKMPF STYKGAERMAILGETAWDFSGVGLFTSLGKAVHGVFSGVYTTMFGVSGWIRILIGF LVLWIGTNSRNTSMATCIAGVGITLPLGFTVQADMGCVCVWSGRELKCSGIFVVDN VHTWTQYKQFESPARLASAILNAHKDGVCGITRSTRLNVMVMKQITNELN"

ORIGIN Query Match 89.3%; Score 25; DB 14; Length 2552; Best Local Similarity 89.3%; Pred. No. 0.97; Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28 ||||| ||||| ||||| ||||| ||||| Db 205 CCCATCTCTCAGAATCCCTGCTGTGG 178

RESULT 30 AY152108S1/c AY152108S1 2552 bp RNA linear VRL 29-SEP-2003 LOCUS Dengue virus type 4 D4.3_1987 polyprotein precursor, gene, partial cds. DEFINITION ACCESSION AY152108.1 GI:28170968 VERSION 1 of 4 KEYWORDS Dengue virus type 4 (DEN-4) ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group. 1 (bases 1 to 2552) Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003) 12832629

REFERENCE 2 (bases 1 to 2552) Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico 12832629

FEATURES source 1. .2552 /organism="Dengue virus type 4" /mol_type="genomic RNA" /isolate="D4.108_1996CR" /db_xref="taxon:11070" /country="Costa Rica" /note="acronym: DEN-4" 1. .>2552 /note="contains core protein, matrix protein and envelope glycoprotein" /codon_start=1 /product="polyprotein precursor" /protein_id="AAN38391.1" /db_xref="GI:28170966" /translation="MNORKKVVPPFNMLKRRNRVSTPQGLVKRFSTGLFSGKGPLR MVLAFITFLRVLSIPTTAGILKRWGLKQKRAIKILIGPRKEIGRMNLINLGRKRSTI TLLCLIPFWAFHLSTEDGEPLMIVAKHERGRPLLPKTTGINKKTLIANDLGEMCED TVYKCLIPWAFHLSTEDGEPLMIVAKHERGRPLLPKTTGINKKTLIANDLGEMCED RAETWMSSEGLAWKQVSEWILNPGFALLAGFMAYMIGQGTQRTVFFVLMMLVAP SYGMRCVGVGNRDFVEVSGGAWDLVLEHGGCVTTMAQCKPLDPLFTKTAKEVAL LRTYCIASISNITTATRCPTQGEPLKEBQDOQYICRRDVRDVGWNGGGLFGKGV VTCAPKSCSGKITGNLVOIENLEYTVVTVHNGDTHAVNGDTHSHGVTATITPRSPV EVKLPDYBELTDCPEPSGIDENEMILMKKKKTLVHKQFMDLPLPWTAGADTSEV HWYKERMVTFKVPKARQDVTVLGSEGMHSAALAGATEVDSGDGNHMFAGHLKCKV RMEKLRIGMSYTCSCGFSIDKEMASTQHTTVKVKYEGAGAPCKVPIEIRDVNKE KVGVRVISTPLAENTSVNIELEPPGDSYIVIGVNSALTLMHFRKSSIGKMPF STYKGAERMAILGETAWDFSGVGLFTSLGKAVHGVFSGVYTTMFGVSGWIRILIGF LVLWIGTNSRNTSMATCIAGVGITLPLGFTVQADMGCVCVWSGRELKCSGIFVVDN VHTWTQYKQFESPARLASAILNAHKDGVCGITRSTRLNVMVMKQITNELN"


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ORIGIN
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ORIGIN

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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTGG 178
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VERSION AY152120.1 GI:28170995
KEYWORDS
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SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
LOCATION/Qualifiers
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ORIGIN

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Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTGG 178
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DEFINITION Dengue virus type 4 D4.80_1994 polyprotein precursor, gene, partial cds.
ACCESSION AY152124
VERSION AY152124.1 GI:28171004
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
LOCATION/Qualifiers
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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 205 CCCATCTCTCAGAAATCCCTGCTGTGG 178

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DEFINITION Dengue virus type 4 D4.78_1994 polyprotein precursor, gene, partial cds.
ACCESSION AY152128
VERSION AY152128.1 GI:28171013
KEYWORDS
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SOURCE
ORGANISM
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Dengue virus type 4 (DEN-4)
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett.S.N., Holmes.E.C., Chirivella.M., Rodriguez.D.M.,
Beltran.M., Vorndam.V., Gubler.D.J. and McMillan.W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett.S.N., Holmes.E.C., Chirivella.M., Rodriguez.D.M.,
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ORIGIN
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Db 205 CCCATCTCTCAGAAATCCCTGCTGTGG 178

RESULT 37
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LOCUS AY152136S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.76_1994 polyprotein precursor, gene, partial
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PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
        Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
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            Query Match 89.3%; Score 25; DB 14; Length 2552;
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Qy 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
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RESULT 40
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LOCUS AY152152S1
DEFINITION Dengue virus type 4 D4.87.1994 polyprotein precursor, gene, partial
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VERSION AY152152.1 GI:28171067
KEYWORDS
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Dengue virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
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        Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
        Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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FEATURES
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 275	17	60.7	201	13	ADQ44846	Adq44846 Myocardia	348	17	60.7	8967	5	AAC87526	Aac87526 Human fac
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c 285	17	60.7	201	13	ADQ44576	Adq44576 Myocardia	358	17	60.7	9009	2	AAV18884	Aav18884 Homo sapi
c 286	17	60.7	201	13	ADQ44577	Adq44577 Myocardia	359	17	60.7	9009	2	AAV18884	Aav18884 Homo sapi
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c 288	17	60.7	201	13	ADQ44444	Adq44444 Myocardia	361	17	60.7	9009	2	AAV18884	Aav18884 Homo sapi
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c 307	17	60.7	2348	8	ACC46288	Acc46288 Human dit	380	17	60.7	12394	4	AAV18177	Aav18177 Human fac
c 308	17	60.7	2446	4	ABL13927	Ab113927 Drosophil	381	17	60.7	12445	3	AAV18177	Aav18177 Human fac
c 309	17	60.7	3268	3	AAC76087	Aac76087 Human ORF	382	17	60.7	15153	12	ADG93315	Adg93315 DEN3 (S1e
c 310	17	60.7	3391	4	ABL22324	Ab122324 Drosophil	383	17	60.7	19640	11	ACN44570	Acn44570 Human gen
c 311	17	60.7	3714	4	ABL06282	Ab106282 Drosophil	384	17	60.7	23640	11	ACN44680	Acn44680 Mouse gen
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DR WPI; 2003-066244/06.
XX
XX New pharmaceutical compositions containing dengue nucleic acids, useful
PT as a vaccine, particularly for inducing a protective immune response in
PT mammalian subjects against the dengue virus infection.
XX
XX Disclosure; Col 17-20; 26pp; English.
PS
XX
XX The invention discloses a pharmaceutical composition capable of inducing
CC an immune response in a mammalian subject, comprising an immunogenic
CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
CC which includes the envelope and membrane (Brem) genes of a dengue type 1,
CC 2, 3, or 4 virus. Dengue virus (DENV) belongs to the flavivirus genus of
CC the family Flaviviridae and is a positive strand RNA virus encoding ten
CC proteins. These genes are translated as a polypeptide which is cleaved by
CC host and viral proteinases. The virus envelope protein is a major antigen
CC which can be targeted by neutralising antibodies. The membrane protein
CC also appears on the virion surface and is required for proper processing
CC of the envelope protein. Dengue viruses are transmitted primarily by the
CC mosquito, Aedes aegypti, and can lead to human illnesses ranging from
CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and
CC dengue shock syndrome (DSS). Secondary infections, with a different
CC serotype, may lead to an immune enhancement phenomenon. The compositions
CC of the invention are DNA vaccines which are injected into the animal as a
CC technique of gene therapy. The composition is useful as a vaccine,
CC particularly for inducing a protective immune response in mammalian
CC subjects against the dengue virus infection. The sequence presented is
CC the dengue virus type 2 (DENV2) structural gene genome segment
XX
XX Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;
SQ Query Match 89.3%; Score 25; DB 8; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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XX 11-MAR-2004 (first entry)
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XX cellular response; non-structural protein; structural protein;
XX dengue virus serotype; gene; ds; plasmid P2.
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XX WO2003092592-A2.
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XX 13-NOV-2003.
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XX 25-APR-2003; 2003WO-US013279.
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XX 03-MAY-2002; 2002US-0377860P.
XX 23-DEC-2002; 2002US-0436500P.
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XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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XX Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
XX Hanley K;
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XX WPI; 2004-022612/02.
DR

DR P-PSDB; ADG93320.
XX
XX New tetravalent vaccine containing a common nucleotide deletion in the 3'
PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT of disease in humans caused by dengue virus, or for inducing immune
XX response.
XX
XX Disclosure; SEQ ID NO 52; 181pp; English.
PS
XX
XX This invention relates to a novel immunogenic composition being
CC tetravalent and containing a common nucleotide deletion in the 3'
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC structural proteins present in each dengue virus serotype. The present
CC sequence is that of the DEN1 ME chimeric region DNA which is related to
CC the invention.
XX
XX Sequence 2423 BP; 747 A; 513 C; 636 G; 527 T; 0 U; 0 Other;
SQ Query Match 89.1%; Score 25; DB 12; Length 2423;
Best Local Similarity 89.3%; Pred. No. 0.41;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 306 CCCATCTCTCAGATCCCTGCTGTGG 279

RESULT 5
AAD53912/c
ID AAD53912 standard; DNA; 10616 BP.
XX
XX AAD53912;
XX
XX 28-MAY-2003 (first entry)
XX
XX Dengue virus type 2 strain rDEN2/4delta30 DNA.
XX
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
XX Dengue virus.
XX
XX Location/Qualifiers
XX Key 97..10263
XX CDS /*tag= a
XX /*product= "DEN4 strain rDEN2/4delta30 protein"
XX mat_peptide 97..438
XX /*tag= c
XX /*product= "Anchored capsid protein"
XX mat_peptide 97..396
XX /*tag= b
XX /*product= "Virion capsid protein"
XX mat_peptide 439..936
XX /*tag= d
XX /*product= "Membrane precursor protein"
XX mat_peptide 712..936
XX /*tag= e
XX /*product= "Membrane protein"
XX mat_peptide 937..2421
XX /*tag= f
XX /*product= "Envelope protein"
XX mat_peptide 2422..3477
XX /*tag= g
XX /*product= "NS1 protein"
XX mat_peptide 3478..4131
```

```

FT FT      /*tag= h
FT FT      /product= "NS2A protein"
FT FT      4132.4521
FT FT      /*tag= i
FT FT      /product= "NS2B protein"
FT FT      4522.6375
FT FT      /*tag= j
FT FT      /product= "NS3 protein"
FT FT      6376.6756
FT FT      /*tag= k
FT FT      /product= "NS4A protein"
FT FT      6757.6825
FT FT      /*tag= l
FT FT      /product= "2K protein"
FT FT      6826.7560
FT FT      /*tag= m
FT FT      /product= "NS4B protein"
FT FT      7561.10260
FT FT      /*tag= n
FT FT      /product= "NS5 protein"
XX
XX WO200295075-A1.
PN
XX
XX
XX 28-NOV-2002.
PD
XX
XX 22-MAY-2002; 2002WO-US016308.
PF
XX
XX 22-MAY-2001; 2001US-0293049P.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35314.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 135-138; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX phenotype in which the viral genome is modified by introduction of a
XX mutation, singly or in combination, taken from mutations from recombinant
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX dengue type 4 virus. The methods and compositions of the invention are
XX useful for fine tuning the attenuation and growth characteristics of
XX dengue virus vaccines for the prevention and/or treatment of dengue virus
XX infection. The present sequence is Dengue virus type 4 strain
XX rDEN2/4delta30 DNA
XX
XX Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
XX
XX Query Match      89.3%; Score 25; DB 10; Length 10616;
XX Best Local Similarity 89.3%; Pred. No. 0.52;
XX Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy      1 CCCATCTCTCANNATCCCTGCTGTGG 28
XX      |||||
XX Db      304 CCCATCTCTTCAGTATCCCTGCTGTGG 277
XX
XX RESULT 6
XX AAD53911/c
XX ID AAD53911 standard; DNA; 10649 BP.
XX
XX AC AAD53911;
XX
XX DT 28-MAY-2003 (first entry)
XX
DE Recombinant dengue virus type 4 strain rDEN4 DNA.
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
XX Dengue virus.
XX
XX Key Location/Qualifiers
XX CDS 102..10649
XX
XX FT      /*tag= a
XX FT      /product= "DEN4 strain rDEN4 protein"
XX FT      102..440
XX FT      /*tag= c
XX FT      /product= "Anchored capsid protein"
XX FT      102..398
XX FT      /*tag= b
XX FT      /product= "Virion capsid protein"
XX FT      441..938
XX FT      /*tag= d
XX FT      /product= "Membrane precursor protein"
XX FT      714..938
XX FT      /*tag= e
XX FT      /product= "Membrane protein"
XX FT      939..2423
XX FT      /*tag= f
XX FT      /product= "Envelope protein"
XX FT      2424..3479
XX FT      /*tag= g
XX FT      /product= "NS1 protein"
XX FT      3480..4133
XX FT      /*tag= h
XX FT      /product= "NS2A protein"
XX FT      4134..4523
XX FT      /*tag= i
XX FT      /product= "NS2B protein"
XX FT      4524..6377
XX FT      /*tag= j
XX FT      /product= "NS3 protein"
XX FT      6378..6758
XX FT      /*tag= k
XX FT      /product= "NS4A protein"
XX FT      6638..7562
XX FT      /*tag= m
XX FT      /product= "NS4B protein"
XX FT      6759..6827
XX FT      /*tag= l
XX FT      /product= "2K protein"
XX FT      7563..10262
XX FT      /*tag= n
XX FT      /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35313.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 131-132; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a

```

CC phenotype in which the viral genome is modified by introduction of a
CC mutation, singly or in combination, taken from mutations from recombinant
CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
CC mutations of dengue type 4 virus (DENV4) or mutations known to attenuate
CC dengue type 4 virus. The methods and compositions of the invention are
CC useful for fine tuning the attenuation and growth characteristics of
CC dengue virus vaccines for the prevention and/or treatment of dengue virus
CC infection. The present sequence is Dengue virus type 4 strain rDENV4 DNA
XX
SQ Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 10; Length 10649;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 306 CCCATCTCTCAGAAATCCCTGCTGTGG 279

RESULT 7
AAD53910/C
ID AAD53910 standard; DNA; 10649 BP.
XX AC
XX AAD53910;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dengue virus type 4 strain 2A DNA.
XX
KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
OS Dengue virus.
XX
FH Key Location/Qualifiers
FT CDS 102..10649
FT /*tag= a
FT /product= "DENV4 strain 2A protein"
FT 102..440
FT /*tag= c
FT /product= "Anchored capsid protein"
FT 102..398
FT /*tag= b
FT /product= "Viron capsid protein"
FT 441..938
FT /*tag= d
FT /product= "Membrane precursor protein"
FT 714..938
FT /*tag= e
FT /product= "Membrane protein"
FT 939..2423
FT /*tag= g
FT /product= "NS1 protein"
FT 2424..3479
FT /*tag= f
FT /product= "Envelope protein"
FT 3480..4133
FT /*tag= h
FT /product= "NS2A protein"
FT 4134..4523
FT /*tag= i
FT /product= "NS2B protein"
FT 4524..6377
FT /*tag= j
FT /product= "NS3 protein"
FT 6378..6758
FT /*tag= k
FT /product= "NS4A protein"
FT 6759..6827
FT /*tag= l
FT /product= "2K protein"
FT 6828..7562
FT /*tag= m

FT mat_peptide /product= "NS4B protein"
FT 7563..10262
FT /*tag= n
FT /product= "NS5 protein"
XX
PN WO200295075-A1.
XX
PD 28-NOV-2002.
XX
PF 22-MAY-2002; 2002WO-US016308.
XX
PR 22-MAY-2001; 2001US-0293049P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (BLAN/) BLANEY J E.
XX
PI Whitehead SS, Murphy BR, Hanley KA;
XX
DR WPI; 2003-120809/11.
DR P-PSDB; AAE35312.
XX
PT New mutated flavivirus, useful for fine tuning the attenuation and growth
PT characteristics of dengue virus vaccines for the prevention and/or
PT treatment of dengue virus infection.
XX
PS Disclosure; Page 123-126; 246pp; English.
XX
CC The present invention relates to novel mutated flaviviruses comprising a
CC phenotype in which the viral genome is modified by introduction of a
CC mutation, singly or in combination, taken from mutations from recombinant
CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
CC mutations of dengue type 4 virus (DENV4) or mutations known to attenuate
CC dengue type 4 virus. The methods and compositions of the invention are
CC useful for fine tuning the attenuation and growth characteristics of
CC dengue virus vaccines for the prevention and/or treatment of dengue virus
CC infection. The present sequence is Dengue virus type 4 strain 2A DNA
XX
SQ Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 10; Length 10649;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 306 CCCATCTCTCAGAAATCCCTGCTGTGG 279

RESULT 8
AAD14605/C
ID AAD14605 standard; cDNA; 10717 BP.
XX
AC AAD14605;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DENV)-2/3-VP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS Dengue virus; type III.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10266
FT /*tag= a
FT /product= "DEN-2/3-VP1 fusion protein"
XX
PN WO200160847-A2.
XX

PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07984.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 2; Page 203-219; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present CDNA
XX sequence encodes dengue virus (DEN)-2/3-VPI fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
XX type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10717;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 9
AAT49303/C
ID AAT49303 standard; cDNA; 10723 BP.
XX
XX AAT49303;
XX
XX 27-AUG-2003 (revised)
DT 11-SEP-1997 (first entry)
XX
XX cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX DHF; DSS; ss.
XX
XX Dengue virus type 2 (strain 16681).
XX
XX Key Location/Qualifiers
FH 97. .10272
FT /tag= a
FT /product= "DEN-2 polyprotein
FT /transl except (pos:9208..9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
XX

PN WO9640933-A1.
XX
PD 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06590.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 23; Page 107-121; 261pp; English.
XX
XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
XX The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, PDK
XX NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
XX -53, may be used in the production of a quadravalent vaccine which
XX provides immunity against all four serotypes of dengue virus. The vaccine
XX also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
XX a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
XX protect against infection by all four serotypes of dengue virus, DEN-1,
XX DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
XX haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
XX to produce the recombinant protein products of the DNA constructs which
XX are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;

Query Match 89.3%; Score 25; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 10
AAT49304/C
ID AAT49304 standard; cDNA; 10723 BP.
XX
XX AAT49304;
XX
XX 27-AUG-2003 (revised)
DT 12-SEP-1997 (first entry)
XX
XX cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX DHF; DSS; ss.
XX
XX Dengue virus type 2 (strain 16681).
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 57
FT mutation /tag= b
FT /note= "C>T mutation"
FT CDS 97. .10272
FT /tag= a

FT FT /product= "DEN-2 attenuated polyprotein
FT FT /transl_except(pos:643..645, aa:Xaa)
FT FT /transl_except(pos:1135..1137, aa:Xaa)
FT FT /transl_except(pos:1393..1395, aa:Xaa)
FT FT /transl_except(pos:2809..2811, aa:Xaa)
FT FT /transl_except(pos:3040..3042, aa:Xaa)
FT FT /transl_except(pos:9208..9210, aa:Xaa)"
FT FT /note= "Xaa = unknown amino acid"
FT FT 524
FT FT /*tag= C
FT FT /note= "A>T mutation, causes Asp to Val substitution"
FT FT 2055
FT FT /*tag= d
FT FT /note= "C>T mutation"
FT FT 2579
FT FT /*tag= e
FT FT /note= "G>A mutation, causes Gly to Asp substitution"
FT FT 4018
FT FT /*tag= f
FT FT /note= "C>T mutation, causes Leu to Phe substitution"
FT FT 5547
FT FT /*tag= g
FT FT /note= "C>T mutation"
FT FT 6599
FT FT /*tag= h
FT FT /note= "G>C mutation, causes Gly to Ala substitution"
FT FT 8571
FT FT /*tag= i
FT FT /note= "C>T mutation"
FT FT
FT FT WO9640933-A1.
FT FT
FT FT 19-DEC-1996.
FT FT
FT FT 06-JUN-1996; 96WO-US009209.
FT FT
FT FT 07-JUN-1995; 95US-00483292.
FT FT
FT FT (USSH) US DEPT HEALTH & HUMAN SERVICES.
FT FT (UYMA-) UNIV MAHIDOL AT SALAYA.
FT FT
FT FT Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
FT FT Kinney R, Trent DW;
FT FT WPI: 1997-052330/05.
FT FT P-PSDB; AAW06591.
FT FT
FT FT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
FT FT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
FT FT quadravalent vaccine for protecting against Dengue virus infection.
FT FT
FT FT Claim 27; Page 122-136; 261pp; English.
FT FT
FT FT This sequence encodes the polyprotein from an attenuated derivative of
FT FT Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
FT FT polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
FT FT NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
FT FT production of a quadravalent vaccine which provides immunity against all
FT FT four serotypes of dengue virus. The vaccine also comprises a chimeric DEN
FT FT -2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
FT FT The new quadravalent vaccines are used to protect against infection by
FT FT all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
FT FT can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
FT FT syndrome (DHF/DSS). Host cells are used to produce the recombinant
FT FT protein products of the DNA constructs which are used in the vaccines.
FT FT (Updated on 27-AUG-2003 to correct OS field.)
FT FT
FT FT SQ Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;

Query Match 89.3%; Score 25; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.52; Mismatches 0; Indels 3; Gaps 0;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTTGG 28
Db 304 CCCATCTCTTCAATATCCCTGCTGTTGG 277
RESULT 11
AAD14614/c
ID AAD14614 standard; cDNA; 10723 BP.
XX
XX AAD14614;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VP1 chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infectious; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
OS Dengue virus; type II.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2/1-VP1 fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI: 2001-497162/54.
DR P-PSDB; AAE07993.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 5; Page 422-438; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.52; Mismatches 0; Indels 3; Gaps 0;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTTGG 28

Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 14

AAD14608/c

ID AAD14608 standard; cDNA; 10723 BP.

AC AAD14608;

XX 01-NOV-2001 (first entry)

XX Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.

XX Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; muten;

XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;

XX ss.

XX Dengue virus; type II.

OS Synthetic.

XX Key Location/Qualifiers

FT mutation replace(57, C)

FT /*tag= b

XX CDS 97..10272

FT /*tag= a

FT /product= "DEN-2 PDK-53 protein variant"

FT mutation replace(524, A)

FT /*tag= c

FT mutation replace(2055, C)

FT /*tag= d

FT mutation replace(2579, G)

FT /*tag= e

FT mutation replace(4018, C)

FT /*tag= f

FT mutation replace(5270, A)

FT /*tag= g

FT mutation replace(5547, T)

FT /*tag= h

FT mutation replace(6599, G)

FT /*tag= i

FT mutation replace(8571, C)

FT /*tag= j

XX WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07987.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for

XX vaccinating against a range of dengue viruses.

XX Example 1; Page 276-292; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras

XX comprising amino acid mutations in the non-structural proteins of a

XX flavivirus. Chimeric viruses containing the attenuation-mutated non-

XX structural genes of the virus are used as a backbone into which the

XX structural protein genes of a second flavivirus strain are inserted.

XX These chimeric viruses elicit pronounced immunogenicity but lack the

XX accompanying clinical symptoms of viral disease. Attenuated chimeric

XX flaviviruses are combined in a pharmaceutical composition to confer

XX simultaneous immunity against several strains of pathogenic flaviviruses

XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic

CC flavivirus chimeras are also used as immunogens or multivalent vaccines

CC to confer simultaneous protection against infections. The present cDNA

CC sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant

CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1

CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome

CC contains 5' non-coding region followed by a capsid protein (C) encoding

CC region, (E) encoding protein (prM) encoding region, an envelope

CC protein, (E) encoding region, followed by the region encoding non-

CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'

CC non-coding region

XX

SQ Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10723;

Best Local Similarity 89.3%; Pred. No. 0.52;

Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTTCANNATCCCTGCTGTGG 28

Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 15

ADN98025/c

ID ADN98025 standard; DNA; 10724 BP.

XX ADN98025;

XX 29-JUL-2004 (first entry)

XX Dengue Virus isolate New Guinea complete genome sequence.

DE ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;

KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.

XX Dengue virus.

XX WO2004040263-A2.

XX 13-MAY-2004.

XX 31-OCT-2003; 2003WO-US034823.

XX 31-OCT-2002; 2002US-0422755P.

XX 06-JUN-2003; 2003US-0476513P.

XX (HEAL-) HEALTH RES INC.

XX Wong SJ, Pei-Yong S;

XX WPI; 2004-400223/37.

XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein

XX reactive with antibody against WNV and cross-reactive with antibody

XX against a flavivirus, useful in diagnosing flavivirus infection caused by

XX DENV, WNV, JEV or SLEV.

XX Disclosure; Fig 40; 212pp; English.

XX The invention relates to a diagnostic kit comprising at least one

XX isolated and purified polypeptide comprising a West Nile Virus (WNV)

XX envelope (E) protein or its immunogenic fragment having a native

XX conformation or non-denatured structure and that is reactive with

XX antibodies against WNV and cross-reactive with antibodies against a

XX flavivirus. The diagnostic kit is useful in diagnosing flavivirus

XX infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to

XX the complete nucleotide sequence of the DENV isolate New Guinea.

XX

SQ Sequence 10724 BP; 3542 A; 2212 C; 2725 G; 2245 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 12; Length 10724;

Best Local Similarity 89.3%; Pred. No. 0.52;

Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 16
AAD14609/c
ID AAD14609 standard; cDNA; 10756 BP.
XX
AC AAD14609;
XX
DT 11-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/WN-PP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS West Nile virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10305
FT FT /tag= a
FT FT /product= "DEN-2/WN-PP1 fusion protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
DR WPI; 2001-497162/54.
DR P-PSDB; AAE07988.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 6; Page 300-316; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/WN-PP1 fusion protein related to
CC the invention. This fusion protein contains DEN-2 16681 backbone and the
CC premembrane/membrane protein (ppm) and an envelope protein (E) from West
CC Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-
CC SEP-2003 to standardise OS field)
XX
SQ Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10756;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 17
AAT75919/c
ID AAT75919 standard; DNA; 32 BP.
XX
AC AAT75919;
XX
DT 15-SEP-1997 (first entry)
XX
DE DEN-2 cloning/sequencing sense primer, D2-274.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
XX
OS Synthetic.
XX
PN WO9640933-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US009209.
XX
PR 07-JUN-1995; 95US-00483292.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
PI Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX
DR WPI; 1997-052330/05.
XX
PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
PS Example; Page 100; 261pp; English.
XX
CC The sequences given in AAT75909-T76029 are primers which were used in the
CC amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the
CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises
CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.
CC The quadravalent vaccine of the invention comprises an attenuated Dengue
CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3
CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are
CC used to protect against infection by all four serotypes of dengue virus,
CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal
CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are
CC used to produce the recombinant protein products of the DNA constructs
CC which are used in the vaccines
XX
SQ Sequence 32 BP; 12 A; 7 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 83.6%; Score 23.4; DB 2; Length 32;
Best Local Similarity 85.7%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 31 CCCATCTCTTCAATATCCCTGCTGTGG 4

RESULT 18
AAD14612/c
ID AAD14612 standard; cDNA; 10648 BP.

```
XX AC AAD14612;
XX AC
XX DT 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX DE Wild-type, virulent DEN-4 1036 cDNA.
XX KW Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
XX KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX OS Dengue virus; type IV.
XX FH Key Location/Qualifiers
XX FT CDS 102..10265
XX FT /*tag= a
XX FT /product= "DEN-4 1036 protein"
XX PN WO200160847-A2.
XX PD 23-AUG-2001.
XX PF 16-FEB-2001; 2001WO-US005142.
XX PR 16-FEB-2000; 2000US-0182829P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX DR P-PSDB; AAE07991.
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX PT vaccinating against a range of dengue viruses.
XX PS Example 3; Page 373-389; 470pp; English.
XX CC The invention relates to avirulent, immunogenic flavivirus chimeras
XX CC comprising amino acid mutations in the non-structural proteins of a
XX CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX CC structural genes of the virus are used as a backbone into which the
XX CC structural protein genes of a second flavivirus strain are inserted.
XX CC These chimeric viruses elicit pronounced immunogenicity but lack the
XX CC accompanying clinical symptoms of viral disease. Attenuated chimeric
XX CC flaviviruses are combined in a pharmaceutical composition to confer
XX CC simultaneous immunity against several strains of pathogenic flaviviruses
XX CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX CC flavivirus chimeras are also used as immunogens or multivalent vaccines
XX CC to confer simultaneous protection against infections. The present cDNA
XX CC sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
XX CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX CC contains 5' non-coding region followed by a capsid protein (C) encoding
XX CC region, premembrane/membrane protein (prM) encoding region, an envelope
XX CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
XX CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX SQ Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
Query Match 83.6%; Score 23.4; DB 4; Length 10648;
Best Local Similarity 85.7%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 1 CCCATCTCTCCTCANNATCCCTCTCTTGG 28
| | | | | | | | | | | | | | | |
Db 306 CCCATCTCTTTCAGAAATCCCTCTCTTGG 279
| | | | | | | | | | | | | | | |
RESULT 19
AAD14613/c
ID AAD14613 standard; cDNA; 10648 BP.
XX AC AAD14613;
XX AC
XX DT 01-NOV-2001 (first entry)
XX DE Attenuated, vaccine-strain DEN-4 PDK-48 variant cDNA.
XX KW Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; mutein;
XX KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX OS Dengue virus; type IV.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT CDS 102..10265
XX FT /*tag= a
XX FT /product= "DEN-4 PDK-48 protein variant"
XX FT mutation replace(1211, T)
XX FT mutation replace(1971, G)
XX FT mutation replace(3182, G)
XX FT mutation replace(6660, C)
XX FT mutation replace(6957, A)
XX FT mutation replace(7162, T)
XX FT mutation replace(7546, C)
XX FT mutation replace(7623, G)
XX FT mutation replace(7623, G)
XX PN WO200160847-A2.
XX PD 23-AUG-2001.
XX PF 16-FEB-2001; 2001WO-US005142.
XX PR 16-FEB-2000; 2000US-0182829P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX DR P-PSDB; AAE07992.
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX PT vaccinating against a range of dengue viruses.
XX PS Example 4; Page 397-413; 470pp; English.
XX CC The invention relates to avirulent, immunogenic flavivirus chimeras
XX CC comprising amino acid mutations in the non-structural proteins of a
XX CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX CC structural genes of the virus are used as a backbone into which the
XX CC structural protein genes of a second flavivirus strain are inserted.
XX CC These chimeric viruses elicit pronounced immunogenicity but lack the
XX CC accompanying clinical symptoms of viral disease. Attenuated chimeric
XX CC flaviviruses are combined in a pharmaceutical composition to confer
XX CC simultaneous immunity against several strains of pathogenic flaviviruses
XX CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX CC flavivirus chimeras are also used as immunogens or multivalent vaccines
XX CC to confer simultaneous protection against infections. The present cDNA
XX CC sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant
XX CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX CC contains 5' non-coding region followed by a capsid protein (C) encoding
XX CC region, premembrane/membrane protein (prM) encoding region, an envelope
XX CC protein (E) encoding region, followed by the region encoding non-
XX CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
XX CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX SQ Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
Query Match 83.6%; Score 23.4; DB 4; Length 10648;
Best Local Similarity 85.7%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 1 CCCATCTCTCCTCANNATCCCTCTCTTGG 28
| | | | | | | | | | | | | | | |
Db 306 CCCATCTCTTTCAGAAATCCCTCTCTTGG 279
| | | | | | | | | | | | | | | |
RESULT 19
AAD14613/c
ID AAD14613 standard; cDNA; 10648 BP.
```

CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
 CC non-coding region. DEN-4 virus passaged in primary dog kidney (PDK) cells
 CC 48 times is designated as DEN-4 PDK-48 virus

XX Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;
 SQ Query Match 83.6%; Score 23.4; DB 4; Length 10648;
 Best Local Similarity 85.7%; Pred. No. 2.7;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
 ||||| ||| ||||| |||||
 Db 306 CCCATCTCTTTCAGATCCCTGCTGTTGG 279

RESULT 20
 AAQ12787/c
 ID AAQ12787 standard; RNA; 10723 BP.

XX AC AAQ12787;
 XX DT 25-MAR-2003 (revised)
 XX DT 21-NOV-1991 (first entry)
 XX DE Dengue 2 virus genome.
 XX KW dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
 XX OS Dengue virus.

XX FH Location/Qualifiers
 XX CDS 97..10272
 FT /*tag= a
 FT 712..936
 FT /*tag= b
 FT /product= "M protein"
 FT 937..2421
 FT /*tag= c
 FT /product= "E protein"
 FT 2422..3477
 FT /*tag= d
 FT /product= "NS1"
 FT 3478..4131
 FT /*tag= e
 FT /product= "NS2A"
 FT 4132..4518
 FT /*tag= f
 FT /product= "NS2B"
 FT 4519..6375
 FT /*tag= g
 FT /product= "NS3"
 FT 6376..6825
 FT /*tag= h
 FT /product= "NS4a"
 FT 6826..7569
 FT /*tag= i
 FT /product= "NS4B"
 FT 7570..10269
 FT /*tag= j
 FT /product= "NS5"

XX FR2654113-A.
 XX PD 10-MAY-1991.
 XX PP 09-NOV-1989; 89FR-00914724.
 XX PR 09-NOV-1989; 89FR-00014724.
 XX PA (INSP) INST PASTEUR.
 XX PI Vincent D;

DR WPI; 1991-225002/31.
 DR P-PSDB; AAR13166.
 XX Detection and identification of Flaviviridae in biological sample - by
 FT amplifying consensus sequence then hybridisation opt. followed by typing,
 FT e.g. sequencing amplified prod.
 XX Disclosure; Fig 3; 24pp; French.
 XX The dengue 2 virus is an example of a member of the Flaviviridae which
 CC can be identified using the probe pair of the invention. A species-
 CC specific sequence can be amplified using the claimed oligonucleotides as
 CC primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses
 CC which can be identified include Japanese encephalitis virus and yellow
 CC fever virus. (Updated on 25-MAR-2003 to correct PR field.)
 XX

SQ Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;
 Query Match 83.6%; Score 23.4; DB 2; Length 10723;
 Best Local Similarity 85.7%; Pred. No. 2.7;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
 ||||| ||| ||||| |||||
 Db 304 CCCATCTTTCAGATCCCTGCTGTTGG 277

RESULT 21
 AAT47666/c
 ID AAT47666 standard; cDNA; 3381 BP.

XX AC AAT47666;
 XX DT 17-OCT-2003 (revised)
 XX DT 19-MAY-1997 (first entry)
 XX DE Dengue virus serotype 2 PR159/S1 mutant sequence.
 XX KW DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.
 XX OS Dengue virus; serotype 2.

XX FH Location/Qualifiers
 XX mutation 1216..1218
 FT /*tag= a
 FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
 FT is GAA (Glu) in wild-type PR159"
 FT mutation 1258..1260
 FT /*tag= b
 FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1
 FT is GTG (Val) in wild-type PR159"
 FT mutation 1762..1764
 FT /*tag= c
 FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1
 FT is ATT (Ile) in wild-type PR159"
 FT mutation 1927..1929
 FT /*tag= d
 FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
 FT is AGT (Ser) in wild-type PR159"

XX WO9637221-A1.
 XX PD 28-NOV-1996.
 XX PP 24-MAY-1996; 96WO-US007627.
 XX PR 24-MAY-1995; 95US-00448734.
 XX PR 07-JUN-1995; 95US-00488807.
 XX PR 10-JUL-1995; 95US-00500469.
 XX PA (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
 XX PI Ivy JM, Nakano E, Clements D;

XX WPI; 1997-020938/02.
DR P-PSDB; AAW09409.
XX Sub-unit vaccine against flavivirus infection - contg. recombinant
PT envelope protein in secretable form, used for immunising against
PT flavivirus infection.
XX
PS Example 1; Fig 3A-D; 121pp; English.
XX
CC A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
CC shows 4 differences from the wild-type DEN-2 PR159. This results in a
CC conservative mutation in domain B of S1 that may be involved in the
CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA
CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of
CC the virus. The clone can be used to express recombinant secreted
CC polypeptides, comprising portions of the envelope protein (esp. domain B,
CC Gly296-Gly385), in eukaryotic hosts, e.g. Yeast (see also AAT47667 and
CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 77.9%; Score 21.8; DB 2; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTCTTTTAATATCCCTGCTGTGG 181
RESULT 22
AAx25114/c
ID AAX25114 standard; cDNA; 3381 BP.
XX
AC AAX25114;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Dengue virus serotype 2 PR159/S1 viral capsid, pprM, E, NS1 cDNA.
XX
XX Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.
XX
OS Dengue virus; serotype 2.
XX
XX WO9906068-A2.
XX
XX 11-FEB-1999.
XX
XX 27-JUL-1998; 98WO-US015447.
XX
XX 31-JUL-1997; 97US-00904227.
XX
XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX
XX Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;
XX
XX WPI; 1999-153454/13.
DR P-PSDB; AAY05522.
XX
XX Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
PT 80% protein, useful for protecting against flavivirus, especially dengue
PT virus infections.
XX
XX Example 1; Fig 3A-D; 60pp; English.
PS
XX
CC This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins
CC (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
CC strain served as the source for DEN-2 genes used in the invention. A
CC vaccine for protecting against flavivirus infection comprises a dimeric
CC 80% E protein that has been secreted as a recombinant protein from a

CC eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.
CC The dimeric truncated E is formed: (1) by directly linking 2 tandem
CC copies of 80% E via a flexible tether; (2) via the formation of a leucine
CC zipper domain through the homodimeric association of 2 leucine zipper
CC helices each fused to the C-terminus of an 80% E molecule; or (3) via the
CC formation of a non-covalently associated four-helix bundle domain formed
CC upon association of two helix-turn-helix moieties attached to the C-
CC terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
CC efficiently secreted by recombinant cells, are easier to purify than
CC intracellular proteins, and generate a high titer neutralising antibody
CC response. The method is generally applicable to flaviviruses, in
CC particular dengue viruses such as DEN-2, where 80% E comprises amino
CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 77.9%; Score 21.8; DB 2; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTCTTTTAATATCCCTGCTGTGG 181
RESULT 23
ADL98085/c
ID ADL98085 standard; DNA; 3381 BP.
XX
XX AC ADL98085;
XX
DT 18-NOV-2004 (first entry)
XX
DE Dengue virus, DEN-2, partial genome.
XX
XX Dengue virus; DEN-2; ss; Envelope protein; 80% E; membrane protein;
XX capsid protein; NS1 protein; Dengue haemorrhagic fever; DHF;
XX Dengue shock syndrome; DSS; flavivirus; vaccine.
XX
OS Dengue virus type 2; strain PR159/S1.
XX
XX Key Location/Qualifiers
FH 1. .3381
CDS /*tag= a
FT /product= "DEN-2 Capsid-membrane-envelope-NS1 proteins"
FT /partial
FT /note= "No stop codon shown"
XX
XX US2003175304-A1.
XX
XX 18-SEP-2003.
XX
XX 20-SEP-2002; 2002US-00247960.
XX
XX 31-JUL-1997; 97US-00904227.
XX
XX 18-AUG-1999; 99US-00376463.
XX
XX (PETE/) PETERS I D.
XX (COLL/) COLLIER B G.
XX (MCDO/) MCDONELL M.
XX (IVYJ/) IVY J M.
XX (HARA/) HARADA K.
XX
XX Peters ID, Collier BG, McDonnell M, Ivy JM, Harada K;
XX WPI; 2003-898503/82.
DR P-PSDB; ADL98086.
XX
XX Vaccine useful for protection against dengue virus infection, comprises a
XX dimeric 80% envelope, which has been secreted as a recombinantly produced
PT protein from Drosophila Schneider cells.
XX

```

PS Example 1; Fig 3; 31pp; English.
XX
CC The invention relates to a vaccine for protection against Flavivirus
CC infection comprising a dimeric 80% envelope (E), which has been secreted
CC as a recombinantly produced protein from Drosophila Schneider cells and
CC which represents the N-terminal 80% portion of the protein from residue 1
CC -395. Also included are a method for protecting a subject against a
CC Flavivirus, an immunogenic polypeptide comprising a dimeric 80% E, an
CC immunogenic composition for protection against Flavivirus infection
CC comprising the immunogenic polypeptide and a carrier, an immunodiagnostic
CC for detecting Flavivirus comprising the immunogenic polypeptide, a vector
CC host recombinant DNA expression system, a DNA sequence encoding the
CC immunogenic polypeptide and an immunodiagnostic kit for detecting
CC Flavivirus in a test subject. The dimeric 80% E products are envelope
CC proteins of serotypes comprising DEN-1, DEN-2, DEN-3 or DEN-4. The
CC Flavivirus is a dengue virus. The 80% E protein is produced as a dimer by
CC incorporating 2 different kinds of leucine zipper peptides or
CC incorporating a helix-turn-helix peptide, to encourage dimerisation. The
CC vaccine is useful for protection against dengue virus infection (e.g.
CC Dengue haemorrhagic fever, DHF, and Dengue shock syndrome, DSS). The
CC present sequence is the partial genomic sequence of the DEN-2 strain
CC PR159/S1 virus, encoding the capsid, membrane, envelope and NS1 proteins.
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 77.9%; Score 21.8; DB 11; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
DB 208 CCCATCTTTTAAATATATCCCTGCTGTGG 181

RESULT 24
ADQ28715/c
ID ADQ28715 standard; DNA; 3381 BP.
XX
AC ADQ28715;
XX
DT 26-AUG-2004 (first entry)
XX
DE Dengue virus viral capsid, prM, E and NS1 genes.
XX
KW virucide; vaccine; Flavivirus; dimeric 80%E; Drosophila Schneider cell;
KW immunogenic composition; multivalent immunodiagnostic; dengue virus;
KW viral capsid; prM gene; E gene; NS1 gene; ds.
XX
OS Dengue virus.
XX
FH Key Location/Qualifiers
FT CDS 1..3381
FT FT /*tag= a
FT FT /product= "Dengue virus viral capsid, prM, E and NS1
FT FT polyprotein"
XX
XX US6749857-B1.
XX
XX 15-JUN-2004.
XX
XX 18-AUG-1999; 99US-00376463.
XX
XX 31-JUL-1997; 97US-00904227.
XX
XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX
XX Peters ID, Coller BG, McDonnell M, Ivy JM, Harada K;
XX
XX WPI; 2004-438725/41.
XX
XX P-PSDB; ADQ28716.
XX
XX New vaccines for preventing or diagnosing infections caused by dengue
XX virus comprises a therapeutic amount of a dimeric 80%E protein secreted
PT

```

```

PT from Drosophila Schneider cells.
XX
XX Example 1; SEQ ID NO 2; 47pp; English.
XX
CC The invention describes a vaccine that generates a protective,
CC neutralising antibody response to a Flavivirus in a murine host. The
CC vaccine comprises a therapeutic amount of a dimeric 80%E, the dimeric
CC 80%E having been secreted as a recombinantly produced protein from
CC Drosophila Schneider cells, and where 80%E represents the N-terminal 80%
CC portion of the protein from residues 1-395. Also described are: an
CC immunogenic polypeptide comprising the dimeric 80%E cited above; an
CC immunogenic composition that generates a protective, neutralising
CC antibody response to a Flavivirus in a murine host, comprising the above
CC immunogenic polypeptide and a physiological carrier; a multivalent
CC immunodiagnostic kit for the detection of Flavivirus, comprising at least 2
CC of the above immunogenic polypeptides of at least 2 flaviviral serotypes;
CC and an immunodiagnostic kit for the detection of Flavivirus in a test
CC subject, comprising the above immunogenic or multivalent immunodiagnostic
CC polypeptide, a suitable support phase coated with dimeric 80%E, and
CC labeled antibodies immunoreactive to antibodies from the test subject.
CC The composition is useful for preventing or diagnosing infections caused
CC by dengue virus. This sequence encodes Dengue virus gene viral capsid,
CC prM, E and NS1 genes for Dengue virus strain PR159/S1 used as the source
CC of DEN-2 genes for the invention.
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 77.9%; Score 21.8; DB 12; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
DB 208 CCCATCTTTTAAATATATCCCTGCTGTGG 181

RESULT 25
ADG93313/c
ID ADG93313 standard; DNA; 15159 BP.
XX
AC ADG93313;
XX
DT 11-MAR-2004 (first entry)
XX
DE DEN2 (Tonga/74) cDNA plasmid P2.
XX
KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
KW dengue virus; delta30; attenuating mutation; humoral response;
KW cellular response; non-structural protein; structural protein;
KW dengue virus serotype; gene; ds; plasmid P2.
XX
OS Dengue virus type 2.
XX
XX WO2003092592-A2.
XX
XX 13-NOV-2003.
XX
XX 25-APR-2003; 2003WO-US013279.
XX
XX 03-MAY-2002; 2002US-0377860P.
XX
XX 23-DEC-2002; 2002US-0436500P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
XX Hanley K;
XX
XX WPI; 2004-022612/02.
XX
XX P-PSDB; ADG93314.
XX
XX New tetravalent vaccine containing a common nucleotide deletion in the 3'
XX untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT

```

PT of disease in humans caused by dengue virus, or for inducing immune
PT response.
PS Disclosure; SEQ ID NO 46; 181pp; English.
XX This invention relates to a novel immunogenic composition being
CC tetra-valent and containing a common nucleotide deletion in the 3',
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetra-valent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetra-valent vaccine, the new tetra-valent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC) structural proteins present in each dengue virus serotype. The present
CC sequence is that of the DEN2 cDNA plasmid P2 which is related to the
CC invention.
XX
SQ Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;
Query Match 77.9%; Score 21.8; DB 12; Length 15159;
Best Local Similarity 82.1%; Pred. No. 15;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTCTTTTAATATATCCCTGCTGTGG 277
RESULT 26
AA049305/c
ID AAT49305 standard; cDNA; 2394 BP.
XX
AC AAT49305;
XX
XX
DT 27-AUG-2003 (revised)
DT 15-SEP-1997 (first entry)
XX
XX
DE Nucleotide sequence of DEN-1 16007 PDK-13 vaccine virus.
XX
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX DHF; DSS; ss.
XX
OS Dengue virus type 2.
XX
XX W09640933-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06592.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 31; Page 172-176; 261pp; English.

XX This sequence represents the nucleotide sequence of one of the candidate
CC vaccine viruses of the invention. This sequence is based on the
CC nucleotide sequence encoding the polyprotein from dengue 2 virus, strain
CC 16681. The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B,
CC NS3, NS4A, NS4B and NS5 proteins. The quadravalent vaccine of the
CC invention comprises an attenuated Dengue virus clone, PDK-53, and a
CC chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-
CC 2/4 virus. The new quadravalent vaccines are used to protect against
CC infection by all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and
CC DEN-4, which can lead to dengue fever or fatal dengue haemorrhagic
CC fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the
CC recombinant protein products of the DNA constructs which are used in the
CC vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 2394 BP; 752 A; 505 C; 622 G; 515 T; 0 U; 0 Other;
Query Match 72.1%; Score 20.2; DB 2; Length 2394;
Best Local Similarity 78.6%; Pred. No. 57;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 115 CCCATCTAGCCAAATTCCTGCTGTGG 88
RESULT 27
AA051476/c
ID AAQ51476 standard; DNA; 10718 BP.
XX
XX AAQ51476;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-MAY-1994 (first entry)
XX
XX DEN1-S275/90 (ECACC V92042111) .
XX
XX Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock syndrome;
XX DSS; DEN1 polypeptides; ss.
XX
XX Dengue virus type 2.
XX
XX
XX Key Location/Qualifiers
XX CDS 81..10271
XX /tag= a
XX misc_RNA 81..422
XX /tag= b
XX misc_RNA 123..422
XX /label= C
XX /tag= C
XX /label= C'
XX misc_RNA 423..695
XX /tag= d
XX /label= PreM
XX misc_RNA 696..920
XX /tag= e
XX /label= M
XX misc_RNA 921..2402
XX /tag= f
XX /label= E
XX misc_RNA 2403..3464
XX /tag= g
XX /label= NS1
XX misc_RNA 3465..4112
XX /tag= h
XX /label= NS2A
XX misc_RNA 4113..4499
XX /tag= i
XX /label= NS2B
XX misc_RNA 4500..6359
XX /tag= j
XX /label= NS3


```
FT misc_RNA 6360..6809
FT /tag= k
FT /label= NS4A
FT misc_RNA 6810..7556
FT /tag= l
FT /label= NS4B
FT misc_RNA 7557..10268
FT /tag= m
FT /label= NS5
XX
XX WO9322440-A1.
PN XX
PD 11-NOV-1993.
XX
XX 28-APR-1993; 93WO-CA000182.
PF
XX 29-APR-1992; 92GB-00009243.
PR
XX (UYSI-) UNIV SINGAPORE NAT.
PA
XX Tan Y, Fu J, Tan B, Yap E, Chan Y;
PI WPI; 1993-368799/46.
XX P-PSDB; AAR43662.
DR
XX New Dengue virus type 1 strain - used to obtain prods. for detection,
PT diagnosis, vaccines and treatment involving virus.
FT Claim 3; Page 20-34; 55pp; English.
PS
XX DEN1 virus, strain S275/90 was isolated from the serum of a dengue
CC haemorrhagic fever (DHF) patient. RNA was isolated from the virus and
CC used to prepare cDNA encoding DEN1 polypeptides. Dengue Virus Type 1
CC prods. can be used for detection, diagnosis, vaccines (inactivated form)
CC or treatment of DEN1 infections. The sequences given in AA051477-86 are
CC oligonucleotides used to prepare cDNA fragments corresp. to Dengue virus
CC proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 10718 BP; 3419 A; 2226 C; 2769 G; 2304 T; 0 U; 0 Other;
Query Match 72.1%; Score 20.2; DB 2; Length 10718;
Best Local Similarity 78.6%; Pred. No. 72;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 288 CCCATCTAGCCAAATTCCTGCTGTGG 261
RESULT 28
AAD14603/c
ID AAD14603 standard; cDNA; 10723 BP.
XX
XX AAD14603;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VP chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
OS Dengue virus; type II.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 97..10272
FT /tag= a
FT /product= "DEN-2/1-VP fusion protein"
XX

PN WO200160847-A2.
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
PF
XX 16-FEB-2000; 2000US-0182829P.
PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
PI WPI; 2001-497162/54.
XX P-PSDB; AAE07982.
DR
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
FT Example 1; Page 155-170; 470pp; English.
PS
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present CDNA
CC sequence encodes dengue virus (DEN)-2/1-VP fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC capsid protein (C), pre-membrane/membrane protein (prM) and an envelope
CC protein (E) from wild-type DEN-1 16007 virus. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
XX SQ Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 U; 0 Other;
Query Match 72.1%; Score 20.2; DB 4; Length 10723;
Best Local Similarity 78.6%; Pred. No. 73;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTGCCAAATTCCTGCTGTGG 277
RESULT 29
AAD14604/c
ID AAD14604 standard; cDNA; 10723 BP.
XX
XX AAD14604;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VP chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
OS Dengue virus; type II.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 97..10272
FT /tag= a
FT /product= "DEN-2/1-VP fusion protein"
XX
```

```
PN WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07983.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 179-195; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), premembrane/membrane protein (prM) and an envelope
XX protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX SQ Sequence 10735 BP; 3514 A; 2228 C; 2722 G; 2259 T; 0 U; 0 Other;

Query Match 72.1%; Score 20.2; DB 4; Length 10723;
Best Local Similarity 78.6%; Pred. No. 73;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTCTCTTGG 28
Db 304 CCCATCTAGCCAAAATTCCTCTTGG 277

RESULT 30
AAD14602/C
ID AAD14602 standard; cDNA; 10735 BP.
XX
XX AC AAD14602;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA.
XX
XX KW Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; muten;
XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX 88.
XX
XX OS Dengue virus; type I.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX CDS 95..10273
XX
XX FT /*tag= a
XX replace(1541, G)
XX replace(1543, A)
XX replace(1545, G)
XX /*tag= e
XX replace(1567, A)
XX /*tag= f
XX replace(1608, C)
XX /*tag= g
XX replace(2363, A)
XX /*tag= h
XX replace(2695, T)
XX /*tag= i
XX replace(2782, C)
XX /*tag= j
XX replace(5063, G)
XX /*tag= k
XX replace(6048, A)
XX /*tag= l
XX replace(6806, A)
XX /*tag= m
XX replace(7330, A)
XX /*tag= n
XX replace(9445, C)
XX /*tag= o
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07981.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 130-146; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), premembrane/membrane protein (prM) and an envelope
XX protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX SQ Sequence 10735 BP; 3429 A; 2231 C; 2776 G; 2299 T; 0 U; 0 Other;

Query Match 72.1%; Score 20.2; DB 4; Length 10735;
Best Local Similarity 78.6%; Pred. No. 73;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Query Match 72.1%; Score 20.2; DB 4; Length 10735;
Best Local Similarity 78.6%; Pred. No. 73;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```



```
XX 16-DEC-2004 (first entry)
XX
XX Skeletal alpha-actin 3'-end nucleotide fragment.
XX
XX IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
XX TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
XX vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
XX cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX
XX Synthetic.
XX
XX WO2004081040-A2.
XX
XX 23-SEP-2004.
XX
XX 11-MAR-2004; 2004WO-US007295.
XX
XX 12-MAR-2003; 2003US-0454079P.
XX
XX (ADVI-) ADVISYS INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Rabinovsky ED, Draghia-Akli R;
XX
XX WPI; 2004-668935/65.
XX
XX New isolated nucleic acid expression construct having a myogenic
XX promoter, a nucleic acid sequence encoding IGF-Ile, and a 3'UTR, useful
XX for treating diabetes, ischemic heart and cerebrovascular disease.
XX
XX Claim 6; SEQ ID NO 5; 104pp; English.
XX
XX The invention relates to an isolated nucleic acid expression construct
XX comprising a myogenic promoter, a nucleic acid sequence encoding an
XX insulin-like growth factor I (IGF-I) or its functional biological
XX equivalent, and a 3' untranslated region (3'UTR), which has in vivo
XX expression activity for the encoded IGF-I in a tissue. The myogenic
XX promoter in the isolated nucleic acid expression construct comprises a
XX transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
XX 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
XX The expression construct further comprises transfection-facilitating
XX vector system that is a plasmid, a viral vector, a liposome, or a
XX cationic lipid. The isolated nucleic acid expression construct also
XX comprises a transfection-facilitating polypeptide having a charged
XX polypeptide and/or poly-L-glutamate. The construct is useful in a method
XX for stimulating angiogenesis, or stimulating myogenesis, or elevating
XX levels of an angiogenic factor, or stimulating endogenous production of
XX an angiopoietin, or treating a muscular or vascular complications of
XX endothelial growth factor (VEGF) or VEGF receptor. The methods and
XX compositions of the present invention are useful for the prevention
XX and/or treatment of diseases or conditions associated with aberrant
XX expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
XX heart disease, diabetic retinopathy and cerebrovascular disease. The
XX present sequence represents the nucleotide sequence of a skeletal alpha-
XX actin 3'-end fragment, a specific example of the 3'-UTR fragment used in
XX the nucleic acid expression construct of the invention.
XX
XX SQ Sequence 2237 BP; 514 A; 567 C; 569 G; 587 T; 0 U; 0 Other;
XX
XX Query Match 67.1%; Score 18.8; DB 13; Length 2237;
XX Best Local Similarity 80.0%; Pred. No. 2.4e+02;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 4 ATCTGNTCANNATCCCTGCTGTGG 28
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX 1925 ATCTCATCATCCTCCCTGCTGTGG 1949
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
XX RESULT 36
XX ADS73973
XX ID ADS73973 standard; DNA; 5423 BP.
```

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XX ADS73973;
XX
XX 16-DEC-2004 (first entry)
XX
XX Plasmid pAV2001 nucleotide sequence.
XX
XX IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
XX TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
XX vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
XX cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX
XX Synthetic.
XX
XX WO2004081040-A2.
XX
XX 23-SEP-2004.
XX
XX 11-MAR-2004; 2004WO-US007295.
XX
XX 12-MAR-2003; 2003US-0454079P.
XX
XX (ADVI-) ADVISYS INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Rabinovsky ED, Draghia-Akli R;
XX
XX WPI; 2004-668935/65.
XX
XX New isolated nucleic acid expression construct having a myogenic
XX promoter, a nucleic acid sequence encoding IGF-Ile, and a 3'UTR, useful
XX for treating diabetes, ischemic heart and cerebrovascular disease.
XX
XX Claim 11; SEQ ID NO 1; 104pp; English.
XX
XX The invention relates to an isolated nucleic acid expression construct
XX comprising a myogenic promoter, a nucleic acid sequence encoding an
XX insulin-like growth factor I (IGF-I) or its functional biological
XX equivalent, and a 3' untranslated region (3'UTR), which has in vivo
XX expression activity for the encoded IGF-I in a tissue. The myogenic
XX promoter in the isolated nucleic acid expression construct comprises a
XX transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
XX 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
XX The expression construct further comprises transfection-facilitating
XX vector system that is a plasmid, a viral vector, a liposome, or a
XX cationic lipid. The isolated nucleic acid expression construct also
XX comprises a transfection-facilitating polypeptide having a charged
XX polypeptide and/or poly-L-glutamate. The construct is useful in a method
XX for stimulating angiogenesis, or stimulating myogenesis, or elevating
XX levels of an angiogenic factor, or stimulating endogenous production of
XX an angiopoietin, or treating a muscular or vascular complications of
XX endothelial growth factor (VEGF) or VEGF receptor. The methods and
XX compositions of the present invention are useful for the prevention
XX and/or treatment of diseases or conditions associated with aberrant
XX expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
XX heart disease, diabetic retinopathy and cerebrovascular disease. The
XX present sequence represents the nucleotide sequence of a plasmid pAV2001,
XX a specific example of the isolated nucleic acid expression construct of
XX the invention.
XX
XX SQ Sequence 5423 BP; 1219 A; 1475 C; 1474 G; 1255 T; 0 U; 0 Other;
XX
XX Query Match 67.1%; Score 18.8; DB 13; Length 5423;
XX Best Local Similarity 80.0%; Pred. No. 2.7e+02;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 4 ATCTGNTCANNATCCCTGCTGTGG 28
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX 2858 ATCTCATCATCCTCCCTGCTGTGG 2882
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
XX RESULT 37
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AAQ32352
ID AAQ32352 standard; DNA; 5674 BP.
XX
AC AAQ32352;
XX
DT 25-MAR-2003 (revised)
DT 22-APR-1993 (first entry)
XX
XX MAGE-1 nucleic acid.
XX
XX melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
XX tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 3881..4711
XX /*tag= a
XX
XX WO9220356-A1.
XX
XX 26-NOV-1992.
XX
XX 22-MAY-1992; 92WO-US004354.
XX
XX 23-MAY-1991; 91US-00705702.
XX 09-JUL-1991; 91US-00728838.
XX 23-SEP-1991; 91US-00764364.
XX 12-DEC-1991; 91US-00807043.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon T, Van Der Bruggen P, Van Den Eynde B, Van Pel A, De Plaen E;
XX Lurquin C, Chomez P, Traversari C;
XX WPI; 1992-415460/50.
XX
XX Nucleic acid mol. encoding a human tumor rejection antigen precursor -
XX useful as an immunostimulant in a vaccine for treating and preventing
XX cancers, also useful in diagnosis.
XX
XX Disclosure; Page 71-73; 142pp; English.
XX
XX The sequences given in AAQ32352-69 represent a new family of genes
XX referred to as melanoma antigens (MAGE). The cDNAs of this gene family
XX were identified during the isolation of the antigen E gene. The MAGE
XX cDNAs, when tested, did not transfer expression of antigen E, but they
XX did show substantial homology to the antigen E cDNA sequence. The MAGE
XX cDNAs share a certain degree of homology with each other and are expressed
XX in tumor cells including several types of human tumor cells as well as
XX in human tumors. MAGE expression is not restricted to melanomas. MAGE
XX refers to a family of tumor rejection antigen precursors. The antigens
XX resulting from these genes are referred to as MAGE TRAs or melanoma
XX antigen tumor rejection antigens. See also AAQ32351. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 5674 BP; 1277 A; 1644 C; 1568 G; 1185 T; 0 U; 0 Other;
XX
XX Query Match 67.1%; Score 18.8; DB 2; Length 5674;
XX Best Local Similarity 80.0%; Pred. No. 2.8e+02;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 CCCATCTCNCANNATCCCTGCTGT 25
XX 1897 CTCATCTGTGAGAAATCCCTGCTGT 1921
XX
XX RESULT 38
XX AAQ72477
XX ID AAQ72477 standard; DNA; 5674 BP.
XX
XX AC AAQ72477;
XX
XX DT 25-MAR-2003 (revised)
XX DT 22-APR-1993 (first entry)
XX
XX MAGE-1 gene.
XX
XX Tumor rejection antigen; vaccine; cancer; MAGE-1 gene; ss.
XX
XX Homo sapiens.
XX
XX US5925729-A.
XX
XX 20-JUL-1999.
XX
XX 02-MAY-1994; 94US-00142368.
XX
XX

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DT 25-MAR-2003 (revised)
DT 22-JUN-1995 (first entry)
XX
DE Tumour rejection antigen MAGE-1 encoding DNA.
XX
KW Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3; cancer;
KW cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 3881..4711
XX /*tag= a
XX
XX WO9423031-A1.
XX
XX 13-OCT-1994.
XX
XX 17-MAR-1994; 94WO-US002877.
XX
XX 26-MAR-1993; 93US-00037230.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;
XX WPI; 1994-333192/41.
XX
XX New tumour rejection antigen precursor MAGE3 - useful in treatment and
XX diagnosis of cancer.
XX
XX Example 26; Page 59; 105pp; English.
XX
XX AAQ72477 is the DNA sequence which encodes melanoma antigen-1 (MAGE-1).
XX Another melanoma antigen MAGE-3 is encoded by AAQ72470, this is a tumour
XX rejection antigen precursor. Melanomas characterised by the expression of
XX MAGE-3 can be detected, or monitored, by contacting a test sample with an
XX agent that can recognise MAGE-3. The melanoma can be treated by the
XX administration of cytolytic T cells specific for the complex of antigen D
XX (the mature rejection antigen derived from MAGE-3) and a human leucocyte
XX antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 U; 0 Other;
XX
XX Query Match 67.1%; Score 18.8; DB 2; Length 5674;
XX Best Local Similarity 80.0%; Pred. No. 2.8e+02;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 CCCATCTCNCANNATCCCTGCTGT 25
XX 1897 CTCATCTGTGAGAAATCCCTGCTGT 1921
XX
XX RESULT 39
XX AAQ84113
XX ID AAX84113 standard; DNA; 5674 BP.
XX
XX AC AAX84113;
XX
XX DT 08-SEP-1999 (first entry)
XX
XX MAGE-1 gene.
XX
XX Tumour rejection antigen; vaccine; cancer; MAGE-1 gene; ss.
XX
XX Homo sapiens.
XX
XX US5925729-A.
XX
XX 20-JUL-1999.
XX
XX 02-MAY-1994; 94US-00142368.
XX
XX

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PR 23-MAY-1991; 91US-00705702.
PR 09-JUL-1991; 91US-00728838.
PR 23-SEP-1991; 91US-00764365.
PR 12-DEC-1991; 91US-00807043.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Van Der Bruggen P, Traversari C, Lurquin C, Boon T, De Plaen E;
PI Van Fei A, Chomez P, Van Den Eynde B;
XX
DR WPI; 1999-418294/35.
XX
PT New tumour rejection antigen is useful as a vaccine against cancerous
PT diseases.
XX
PS Disclosure; Col 39-46; 58pp; English.
XX
SS This sequence represents the MAGE-1 gene sequence. The invention relates
CC to a tumour rejection antigen sequence that is useful as a tumour
CC rejection antigen for vaccination against cancerous conditions
XX
SQ Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 U; 0 Other;
SQ
Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCATCTCTCANNATCCCTGCTGT 25
DB 1897 CTCATCTGTGAGATCCCTGCTGT 1921
XX
RESULT 40
AAX88055
ID AAX88055 standard; DNA; 5707 BP.
XX
AC AAX88055;
XX
DT 08-SEP-1999 (first entry)
XX
DE Plasmid pIG0335 DNA.
XX
KW Plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ds.
XX
OS Synthetic.
XX
PN US5925564-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-00472809.
XX
PR 06-NOV-1991; 91US-00789919.
PR 09-MAR-1994; 94US-00209846.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI O'malley BW, Demayo RJ, Schwartz RJ;
XX
DR WPI; 1999-418276/35.
XX
PT New expression vector system useful for gene therapy.
XX
PS Disclosure; Fig 17-17F; 67pp; English.
XX
CC This invention describes novel expression vector systems containing RNA
CC stability elements from 3' flanking sequences used for establishing
```

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CC expression of a nucleic acid sequence within a tissue. The vectors also
CC facilitate enhanced expression in tissues and target expression with
CC tissue specificity. The expression vectors can be used to treat diseases
CC through gene therapy by targeting the vector to specific tissues.
CC Diseases that can be treated include muscle atrophy associated with
CC neurological, muscular or systemic disease, aging by causing tissues to
CC express trophic factors, haemophilia by causing tissues to express and
CC secrete clotting factor into the circulation, atherogenesis and
CC atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular
CC disease by causing tissues to express factors involved in tissue
CC metabolism. They can be used to replace genes of inherited genetic
CC defects or acquired hormone deficiencies e.g. diabetes. To transform
CC cells to produce particular proteins or RNA in vitro. To create
CC transgenic animals which can be used for research into human diseases,
CC assessing novel therapeutic methods, assessing the effect of chemical and
CC physical carcinogens and for studying the effect of genes and genetic
CC regulatory elements on livestock improvement. They can be used to induce
CC an immune response. These vectors provide controlled expression of the
CC genes they carry and produce a significantly high level of expression.
CC Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC vectors which causes increased expression
XX
SQ Sequence 5707 BP; 1221 A; 1634 C; 1576 G; 1276 T; 0 U; 0 Other;
SQ
Query Match 67.1%; Score 18.8; DB 2; Length 5707;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4 ATCTCNTCANNATCCCTGCTGTGG 28
DB 3092 ATCTCATCATCCTCCTGCTGTGG 3116
XX
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Search completed: July 31, 2005, 13:54:50
Job time : 236 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:00:46 ; Search time 1717.5 Seconds
(without alignments)
620.553 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccattctcannatccctgtgttg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	72.9	1040	9	AG407066 Mus muscu
2	19.8	70.7	476	9	CL336324 RPCI44_26
3	19.2	68.6	287	2	BB338318 BB338318
4	19.2	68.6	453	8	AO517624 HS 5140_B
5	19.2	68.6	481	5	EX109154 EX109154
6	19.2	68.6	511	7	CN675425 AO963B06
7	19.2	68.6	577	9	CN690447 CGXAB64TH
8	19.2	68.6	646	6	CD443887 EL01N0432
9	19.2	68.6	659	9	AG063981 Pan trogl
10	19.2	68.6	681	9	AG291906 Mus muscu
11	19.2	68.6	740	9	AG345215 Mus muscu
12	19.2	68.6	936	9	CL980943 OslFCC035
13	19.2	68.6	938	9	CG232800 OG2B120TV
14	19.2	68.6	952	9	CG456461 PUIJW63TD
15	19.2	68.6	961	9	CNS06EAJ T3 end of
16	19.2	68.6	1018	9	CG456420 PUIJW63TB
17	19.2	68.6	1139	8	CC187707 CH261-33N
18	19.2	68.6	2314	3	BC026893 Mus muscu
19	18.8	67.1	413	2	BF723268 mab30a01
20	18.8	67.1	445	7	CF546284 lae70c10
21	18.8	67.1	463	4	BI048424 MR4-TN011
22	18.8	67.1	923	9	CL116046 ISB1-63A2
23	18.8	67.1	990	9	AL149041 Anopheles
24	18.8	67.1	1137	9	CL025440 CH216-21K

C 25	18.8	67.1	2185	9	CG755418
26	18.6	66.4	231	2	BF655438
27	18.6	66.4	231	2	BF655438
28	18.6	66.4	239	1	AV361516
29	18.6	66.4	244	7	CV367745
30	18.6	66.4	245	5	BX639040
31	18.6	66.4	274	2	BF440266
32	18.6	66.4	280	2	AW354424
33	18.6	66.4	285	1	AV116369
34	18.6	66.4	297	2	BF600952
35	18.6	66.4	300	2	BF174849
36	18.6	66.4	315	9	CR405165
37	18.6	66.4	348	7	CO727823
38	18.6	66.4	389	2	BF601010
39	18.6	66.4	411	4	BM286538
40	18.6	66.4	413	1	AA068952
41	18.6	66.4	414	1	AI614834
42	18.6	66.4	420	1	AU232945
43	18.6	66.4	421	2	AW477778
44	18.6	66.4	446	6	CD804048
45	18.6	66.4	472	6	CB418067
46	18.6	66.4	484	7	CNS35235
47	18.6	66.4	505	4	BM090019
48	18.6	66.4	540	1	AV665694
49	18.6	66.4	550	7	CF162479
50	18.6	66.4	555	7	CN439608
51	18.6	66.4	564	7	CK772354
52	18.6	66.4	568	8	AQ793162
53	18.6	66.4	594	7	CO880755
54	18.6	66.4	598	1	AI390262
55	18.6	66.4	602	5	BQ790197
56	18.6	66.4	613	7	CK781457
57	18.6	66.4	622	7	CF747473
58	18.6	66.4	625	6	CA371379
59	18.6	66.4	627	8	AZ992829
60	18.6	66.4	628	7	CK972854
61	18.6	66.4	658	7	CV067298
62	18.6	66.4	669	7	CK960154
63	18.6	66.4	677	2	BB478112
64	18.6	66.4	678	7	CK637150
65	18.6	66.4	680	7	CO883546
66	18.6	66.4	687	7	CK780310
67	18.6	66.4	698	7	CO045764
68	18.6	66.4	700	4	BI735720
69	18.6	66.4	706	7	CF747552
70	18.6	66.4	709	7	CNS37855
71	18.6	66.4	710	4	BI736791
72	18.6	66.4	711	6	CD351508
73	18.6	66.4	711	7	CF537633
74	18.6	66.4	721	6	CD351287
75	18.6	66.4	722	5	BQ781110
76	18.6	66.4	733	7	CO565305
77	18.6	66.4	746	7	CN440011
78	18.6	66.4	747	8	BZ214246
79	18.6	66.4	749	7	CNS37649
80	18.6	66.4	750	7	CO045568
81	18.6	66.4	755	6	CA124870
82	18.6	66.4	757	7	CO890629
83	18.6	66.4	765	7	CO566306
84	18.6	66.4	767	6	CD351316
85	18.6	66.4	769	7	CK778686
86	18.6	66.4	776	7	CO453418
87	18.6	66.4	784	7	CO045014
88	18.6	66.4	786	6	CB172826
89	18.6	66.4	793	6	CD643116
90	18.6	66.4	874	7	COS73594
91	18.6	66.4	922	5	B0840377
92	18.6	66.4	2511	3	AK049827
93	18.6	66.4	2562	9	CL962411
94	18.6	66.4	4276	3	AK033268
95	18.6	66.4	4508	3	AK044502
96	18.4	65.7	249	8	B74690
97	18.4	65.7	333	1	AV750001

c 98	18.4	65.7	474	2	AW184935	se83h10.Y	c 171	18.2	65.0	1416	9	CL648708	CH213-191
c 99	18.4	65.7	488	5	BP069231	BP069231	c 172	18.2	65.0	2526	3	AK047577	Mus muscu
c 100	18.4	65.7	508	8	AQ531444	RPCI-11-3	c 173	18	64.3	470	1	AJ828855	AJ828855
c 101	18.4	65.7	633	8	AQ020115	CJT-HSP-2	c 174	18	64.3	612	2	BF664792	602117715
c 102	18.4	65.7	718	7	CF888204	ama8tc-24	c 175	18	64.3	631	1	AL896204	AL896204
c 103	18.2	65.0	255	2	BB497890	BB497890	c 176	18	64.3	656	5	EX770566	EX770566
c 104	18.2	65.0	282	2	BB080784	BB080784	c 177	18	64.3	691	9	CNS03E4R	Tetraodon
c 105	18.2	65.0	320	1	AI821851	nr38e03.x	c 178	18	64.3	713	5	EX779987	EX779987
c 106	18.2	65.0	320	1	AI826991	wk55c07.x	c 179	18	64.3	732	5	BQ028610	QHH1907.Y
c 107	18.2	65.0	320	2	BP855145	RC3-FN020	c 180	18	64.3	866	7	CR421332	CR421332
c 108	18.2	65.0	321	1	AA635855	nr38e03.s	c 181	18	64.3	868	7	CR422895	CR422895
c 109	18.2	65.0	328	1	AI821103	nr38e03.Y	c 182	18	64.3	890	5	EX691574	EX691574
c 110	18.2	65.0	401	9	CE402683	ti9r-g8s-	c 183	17.8	63.6	225	7	CF483205	CF483205
c 111	18.2	65.0	409	4	BG900352	HOA37-1-G	c 184	17.8	63.6	264	1	AV361891	AV361891
c 112	18.2	65.0	463	1	AI972423	w39e06.x	c 185	17.8	63.6	278	7	CF431363	NIT1_5_F0
c 113	18.2	65.0	477	5	EX645883	DRFZP781M	c 186	17.8	63.6	300	1	AV176398	AV176398
c 114	18.2	65.0	478	8	AQ559205	HS_2069.B	c 187	17.8	63.6	300	6	C29822	C29822
c 115	18.2	65.0	490	7	CF139319	UI-HF-CB0	c 188	17.8	63.6	300	6	C33214	C33214
c 116	18.2	65.0	514	7	CF141511	UI-HF-CB0	c 189	17.8	63.6	373	6	BY630265	BY630265
c 117	18.2	65.0	529	8	AQ435078	HS_5114.B	c 190	17.8	63.6	386	6	BY582838	BY582838
c 118	18.2	65.0	543	7	CF860905	peZ0001G	c 191	17.8	63.6	404	6	CA910371	CA910371
c 119	18.2	65.0	548	9	CE632872	ti9r-g8s-	c 192	17.8	63.6	444	2	BB776803	BB776803
c 120	18.2	65.0	559	8	AQ560496	HS_2069.B	c 193	17.8	63.6	456	2	BF411402	BF411402
c 121	18.2	65.0	562	7	CF122893	UI-HF-CB0	c 194	17.8	63.6	472	8	AQ526076	AQ526076
c 122	18.2	65.0	566	7	CF122893	UI-HF-CB0	c 195	17.8	63.6	499	4	BQ749870	BQ749870
c 123	18.2	65.0	572	7	CN975880	25782_125	c 196	17.8	63.6	518	7	CF440110	EST676455
c 124	18.2	65.0	580	7	CN984289	53244_126	c 197	17.8	63.6	520	2	AW564688	LGI_300.B
c 125	18.2	65.0	582	6	CD832213	BN40_062H	c 198	17.8	63.6	532	4	BI502040	km08e07.Y
c 126	18.2	65.0	585	6	CD836930	BN45_050H	c 199	17.8	63.6	533	4	BM141332	BM141332
c 127	18.2	65.0	594	9	CE598373	ti9r-g8s-	c 200	17.8	63.6	551	6	CB521458	CB521458
c 128	18.2	65.0	597	2	BF731559	maB8C08.	c 201	17.8	63.6	554	8	AQ546078	AQ546078
c 129	18.2	65.0	614	6	CA697619	wk4.pK00	c 202	17.8	63.6	571	9	CE448016	CE448016
c 130	18.2	65.0	630	5	BX085619	BX085619	c 203	17.8	63.6	579	6	CA187308	SCUTST309
c 131	18.2	65.0	638	6	CD835575	BN45_045P	c 204	17.8	63.6	613	4	BJ650386	BJ650386
c 132	18.2	65.0	641	5	BX085620	BX085620	c 205	17.8	63.6	616	6	CA108118	SCSBR105
c 133	18.2	65.0	647	9	AG041617	Pan trogl	c 206	17.8	63.6	616	8	BH822692	BH822692
c 134	18.2	65.0	653	2	BE584928	1-11G-ZO	c 207	17.8	63.6	617	6	CA743704	CA743704
c 135	18.2	65.0	654	5	BU238152	De01_13c0	c 208	17.8	63.6	625	7	BF113314	BF113314
c 136	18.2	65.0	661	6	BY733962	Dv733962	c 209	17.8	63.6	626	8	BH835207	BACPP7-N1
c 137	18.2	65.0	672	6	CD355410	UI-M-PY0-	c 210	17.8	63.6	631	6	CA106744	SCQSHR102
c 138	18.2	65.0	676	6	CD837009	BN45_050L	c 211	17.8	63.6	634	6	CA092088	SCUTAN211
c 139	18.2	65.0	678	9	CE119987	ti9r-g8s-	c 212	17.8	63.6	638	7	CF449306	CF449306
c 140	18.2	65.0	687	7	CF146763	UI-HF-CB0	c 213	17.8	63.6	650	8	AZ414986	AZ414986
c 141	18.2	65.0	687	7	CF146837	UI-HF-CB0	c 214	17.8	63.6	666	6	CA914280	PCSC19401
c 142	18.2	65.0	701	6	CF722915	UI-M-GH0-	c 215	17.8	63.6	670	6	CA089948	SCSGAM207
c 143	18.2	65.0	711	7	CF831705	UCRCR01_0	c 216	17.8	63.6	676	6	CB525542	UI-M-FV0-
c 144	18.2	65.0	715	5	BU055491	UI-M-F00-	c 217	17.8	63.6	698	6	CA188826	SCCAM2C0
c 145	18.2	65.0	719	6	CD836858	BN45_050D	c 218	17.8	63.6	710	6	CD210780	CD210780
c 146	18.2	65.0	730	5	BU058588	UI-M-F00-	c 219	17.8	63.6	721	7	CF435437	CF435437
c 147	18.2	65.0	731	6	CD837681	BN45_053D	c 220	17.8	63.6	738	7	CV045059	EST_6766
c 148	18.2	65.0	732	7	CN185552	UCRCS05_0	c 221	17.8	63.6	740	9	AG295387	Mus muscu
c 149	18.2	65.0	737	6	CD837090	BN45_051A	c 222	17.8	63.6	782	9	AX154563	Danio rer
c 150	18.2	65.0	744	9	AG518630	Mus muscu	c 223	17.8	63.6	783	9	EX991431	EX991431
c 151	18.2	65.0	753	6	CB942622	AGENCOURT	c 224	17.8	63.6	794	9	CC919031	CC919031
c 152	18.2	65.0	754	7	CO560325	AGENCOURT	c 225	17.8	63.6	876	8	AZ672551	ENTHC49TR
c 153	18.2	65.0	760	7	CN183954	UCRCS04_0	c 226	17.8	63.6	904	9	CNS03QVT	CNS03QVT
c 154	18.2	65.0	766	9	EX146761	Danio rer	c 227	17.8	63.6	916	2	BF125779	BF125779
c 155	18.2	65.0	772	6	CD835746	BN45_0461	c 228	17.8	63.6	924	2	CNS03HPV	CNS03HPV
c 156	18.2	65.0	784	6	CB521390	UI-M-GH0-	c 229	17.8	63.6	934	9	CBF303KQ	CBF303KQ
c 157	18.2	65.0	796	2	BF234751	602028578	c 230	17.8	63.6	960	2	BF310272	BF310272
c 158	18.2	65.0	801	7	CN537128	UI-M-HS0-	c 231	17.8	63.6	1000	2	CNS05BNN	CNS05BNN
c 159	18.2	65.0	806	2	BB640931	Cr12_1_M1	c 232	17.8	63.6	1044	5	BX380603	BX380603
c 160	18.2	65.0	814	7	CF746305	UI-M-GV0-	c 233	17.8	63.6	1127	7	CK212951	CK212951
c 161	18.2	65.0	818	7	CN187169	UCRCS05_0	c 234	17.8	63.6	1181	6	CD256455	AGENCOURT
c 162	18.2	65.0	850	8	AQ888455	HS_3144A	c 235	17.6	62.9	127	7	CN283098	CN283098
c 163	18.2	65.0	868	1	AU118188	AU118188	c 236	17.6	62.9	185	9	CR181138	CR181138
c 164	18.2	65.0	913	3	CR713394	Tetraodon	c 237	17.6	62.9	228	2	BB150743	BB150743
c 165	18.2	65.0	926	3	CF688659	Tetraodon	c 238	17.6	62.9	228	1	AA755629	AA755629
c 166	18.2	65.0	936	3	CF681377	Tetraodon	c 239	17.6	62.9	272	8	AQ932827	AQ932827
c 167	18.2	65.0	1001	9	CNS05BPQ	Tetraodon	c 240	17.6	62.9	277	8	CE510117	ti9r-g8s-
c 168	18.2	65.0	1101	9	CNS053A3	Tetraodon	c 241	17.6	62.9	280	8	AQ534695	RPCI-23-2
c 169	18.2	65.0	1101	9	CNS0500V	Tetraodon	c 242	17.6	62.9	288	1	AA832894	AA832894
c 170	18.2	65.0	1201	3	CR674997	Tetraodon	c 243	17.6	62.9	288	1	AV311433	AV311433

244	17.6	62.9	295	8	BZ708794	OGEAK07TM	317	17.6	62.9	561	8	AZ900645	RPCI-24-1
C 245	17.6	62.9	297	2	BB092807	BB092807	C 318	17.6	62.9	566	2	BE264616	601192401
C 246	17.6	62.9	308	1	AL678860	AL678860	C 319	17.6	62.9	567	7	CF356892	maJ50602.
C 247	17.6	62.9	313	4	CR774620	CR774620	320	17.6	62.9	567	7	CN297008	170004706
C 248	17.6	62.9	330	7	CR774620	CR774620	321	17.6	62.9	571	4	BJ581270	BJS81270
C 249	17.6	62.9	336	6	CB488304	CB488304	322	17.6	62.9	571	8	AQ883692	HS 5478 B
C 250	17.6	62.9	354	4	BM368760	BM368760	323	17.6	62.9	581	5	AQ883692	HS 5478 B
C 251	17.6	62.9	367	4	BJ185424	BJ185424	324	17.6	62.9	581	5	BP367826	BP367826
C 252	17.6	62.9	377	5	BY072808	BY072808	C 325	17.6	62.9	582	4	BJ160499	BJ160499
C 253	17.6	62.9	385	2	BE102618	BE102618	326	17.6	62.9	582	5	BP304995	BP304995
C 254	17.6	62.9	395	7	W20853	W20853	C 327	17.6	62.9	582	5	BP345651	BP345651
C 255	17.6	62.9	395	2	BE695322	BE695322	C 328	17.6	62.9	584	4	BJ703733	BJ703733
C 256	17.6	62.9	403	4	BJ185880	BJ185880	C 329	17.6	62.9	585	8	AZ298569	RPCI-23-1
C 257	17.6	62.9	409	7	N26768	N26768	329	17.6	62.9	589	4	BJ168746	BJ168746
C 258	17.6	62.9	410	2	AW471015	AW471015	C 330	17.6	62.9	591	7	CN496742	CN496742
C 259	17.6	62.9	424	2	AW443421	AW443421	C 331	17.6	62.9	594	4	BJ203989	BJ203989
C 260	17.6	62.9	425	5	BY449493	BY449493	C 332	17.6	62.9	595	5	BX878488	BX878488
C 261	17.6	62.9	426	2	AW670518	AW670518	333	17.6	62.9	595	6	CB510113	sealwh50
C 262	17.6	62.9	432	1	AI030199	AI030199	C 334	17.6	62.9	602	8	AQ787000	HS 3156 B
C 263	17.6	62.9	432	2	BF742332	BF742332	335	17.6	62.9	603	1	AI988646	EST268089
C 264	17.6	62.9	439	4	EG553669	EG553669	336	17.6	62.9	603	8	AQ527450	RPCI-11-3
C 265	17.6	62.9	440	9	CR833204	CR833204	337	17.6	62.9	607	7	CK617767	m101006.Y
C 266	17.6	62.9	443	4	BI809329	BI809329	338	17.6	62.9	608	9	CR827504	CR827504
C 267	17.6	62.9	447	2	BE020385	BE020385	339	17.6	62.9	609	4	BJ670376	BJ670376
C 268	17.6	62.9	448	1	AV746072	AV746072	340	17.6	62.9	609	4	BJ680048	BJ680048
C 269	17.6	62.9	449	4	BJ159898	BJ159898	C 341	17.6	62.9	609	6	CB006128	VVC030B07
C 270	17.6	62.9	453	2	BB832344	BB832344	C 342	17.6	62.9	610	6	CB005324	VVC011F07
C 271	17.6	62.9	454	6	CB174223	CB174223	C 343	17.6	62.9	610	6	CB005324	CB005324
C 272	17.6	62.9	457	7	CN580920	CN580920	C 344	17.6	62.9	611	1	AI774264	EST255459
C 273	17.6	62.9	457	7	CN580920	CN580920	345	17.6	62.9	611	5	BP766564	BP766564
C 274	17.6	62.9	461	6	CD012422	CD012422	346	17.6	62.9	612	4	BJ593311	BJ593311
C 275	17.6	62.9	470	2	BF602125	BF602125	347	17.6	62.9	612	4	BG063794	H3012H04-
C 276	17.6	62.9	478	4	BJ162329	BJ162329	348	17.6	62.9	613	7	CV105571	AGENCOURT
C 277	17.6	62.9	478	4	BJ645569	BJ645569	C 349	17.6	62.9	614	8	CC432260	PUEGG12TD
C 278	17.6	62.9	480	1	AI899277	AI899277	C 350	17.6	62.9	616	1	AI484751	EST243012
C 279	17.6	62.9	480	1	AI899277	AI899277	C 351	17.6	62.9	617	2	AW991452	RC1-BN000
C 280	17.6	62.9	487	8	AQ810987	AQ810987	C 352	17.6	62.9	622	5	BU261307	603503133
C 281	17.6	62.9	489	2	AS357525	AS357525	353	17.6	62.9	624	4	BJ045677	BJ045677
C 282	17.6	62.9	490	7	CF787790	CF787790	354	17.6	62.9	625	4	BJ581422	BJ581422
C 283	17.6	62.9	491	6	CD013352	CD013352	C 355	17.6	62.9	627	4	BJ176200	BJ176200
C 284	17.6	62.9	493	2	AW251072	AW251072	C 356	17.6	62.9	631	8	BH103391	RPCI-24-3
C 285	17.6	62.9	494	8	CC052388	CC052388	C 357	17.6	62.9	635	4	BI811892	B006B10 O
C 286	17.6	62.9	495	7	CR369447	CR369447	C 358	17.6	62.9	635	4	BM635532	170006875
C 287	17.6	62.9	497	5	BP164740	BP164740	C 359	17.6	62.9	636	5	CD002581	EST00618 N
C 288	17.6	62.9	500	8	B59918	B59918	360	17.6	62.9	636	5	BU364642	603790533
C 289	17.6	62.9	501	4	BI161528	BI161528	C 361	17.6	62.9	643	9	AG131494	Pan trogl
C 290	17.6	62.9	502	1	AA117598	AA117598	C 362	17.6	62.9	647	9	CG2988566	CG2988566
C 291	17.6	62.9	503	7	CK918645	CK918645	C 363	17.6	62.9	648	4	BI295863	UT-R-DK0-
C 292	17.6	62.9	506	5	BQ041243	BQ041243	C 364	17.6	62.9	651	6	CB174279	OR 2039H0
C 293	17.6	62.9	507	4	BI203533	BI203533	365	17.6	62.9	651	7	CN385782	LB2TR0411
C 294	17.6	62.9	507	4	BI207288	BI207288	C 366	17.6	62.9	654	4	BI204681	EST522721
C 295	17.6	62.9	507	4	BI211164	BI211164	C 367	17.6	62.9	655	5	BU425140	603954486
C 296	17.6	62.9	515	4	BJ671149	BJ671149	C 368	17.6	62.9	656	6	CB124937	K-EST0173
C 297	17.6	62.9	517	4	BI294245	BI294245	369	17.6	62.9	657	2	BE251365	601116219
C 298	17.6	62.9	518	8	BZ189347	BZ189347	C 370	17.6	62.9	660	1	AJ453558	AJ453558
C 299	17.6	62.9	521	4	BI193820	BI193820	C 371	17.6	62.9	664	6	CD462263	SAI 40H0
C 300	17.6	62.9	523	1	AI897247	AI897247	C 372	17.6	62.9	666	4	BM717237	UI-E-DW1-
C 301	17.6	62.9	531	6	CB148275	CB148275	C 373	17.6	62.9	666	5	BU041797	PP Lira001
C 302	17.6	62.9	534	6	CB174541	CB174541	C 374	17.6	62.9	667	1	AI748769	8B61905.Y
C 303	17.6	62.9	535	6	BI150261	BI150261	C 375	17.6	62.9	668	4	BI285605	UI-R-CW0-
C 304	17.6	62.9	540	4	BM483882	BM483882	C 376	17.6	62.9	670	2	BE251294	601107804
C 305	17.6	62.9	540	7	CK36213	CK36213	C 377	17.6	62.9	671	4	BJ078278	BJ078278
C 306	17.6	62.9	540	8	BZ868106	BZ868106	C 378	17.6	62.9	672	7	CO237732	W80073.B2
C 307	17.6	62.9	542	1	AA041112	AA041112	C 379	17.6	62.9	673	2	BE267182	601190545
C 308	17.6	62.9	545	4	BJ695231	BJ695231	C 380	17.6	62.9	673	5	BX666297	BX666297
C 309	17.6	62.9	550	5	BP266903	BP266903	C 381	17.6	62.9	673	8	AQ345577	RPCI11-11
C 310	17.6	62.9	551	8	AZ587888	AZ587888	C 382	17.6	62.9	675	6	CA483164	LUP12006E
C 311	17.6	62.9	553	1	AU279438	AU279438	C 383	17.6	62.9	680	5	BU117314	603138774
C 312	17.6	62.9	554	5	BP266570	BP266570	C 384	17.6	62.9	682	2	BB180184	BB180184
C 313	17.6	62.9	554	7	CK547931	CK547931	C 385	17.6	62.9	682	7	CK759065	atR02-1ms
C 314	17.6	62.9	557	6	CD711716	CD711716	C 386	17.6	62.9	683	4	BJ170166	BJ170166
C 315	17.6	62.9	559	2	BF203599	BF203599	C 387	17.6	62.9	683	5	BX866678	BX866678
C 316	17.6	62.9	560	2	AW373824	AW373824	C 388	17.6	62.9	683	8	BZ153963	CH230-396
							C 389	17.6	62.9	685	4	BG077234	H3012H04 -

C 390	17.6	62.9	689	2	BF239512	601906604	463	17.6	62.9	891	5	BM919599	BM919599	AGENCOURT	
C 391	17.6	62.9	691	4	BM140272	OHC-65 Ge	464	17.6	62.9	891	9	CG297942	CG297942	OG3DY43TH	
C 392	17.6	62.9	694	4	BJ603137	BJ603137	C 465	17.6	62.9	896	9	CG305429	CG305429	OGWAB90TV	
C 393	17.6	62.9	694	9	CG678743	ZMWBBC029	C 466	17.6	62.9	901	5	BQ943305	AGENCOURT	BQ943305	
C 394	17.6	62.9	698	5	BP705132	BP705132	C 467	17.6	62.9	907	2	BF311349	AGENCOURT	BF311349	
C 395	17.6	62.9	699	7	CN385777	LE2TRO410	468	17.6	62.9	912	4	EG394469	AGENCOURT	EG394469	
C 396	17.6	62.9	700	1	AI1486585	EST244906	469	17.6	62.9	917	9	CG114753	PJUFN33TD	CG114753	
C 397	17.6	62.9	703	4	BJ592856	BJS92856	470	17.6	62.9	918	9	CG242324	OGW1Q24TH	CG242324	
C 398	17.6	62.9	704	8	CC170157	AI13A10 H	471	17.6	62.9	923	9	CNS02V5S	Tetraodon	AL215353	
C 399	17.6	62.9	706	4	BM347074	AI13A10 H	472	17.6	62.9	924	9	CG121032	GR_EB02A	CO121032	
C 400	17.6	62.9	707	8	CC170445	AI13A10 H	473	17.6	62.9	927	7	CO121032	AGENCOURT	BQ925134	
C 401	17.6	62.9	709	6	BY755552	BY755552	474	17.6	62.9	931	5	BQ925134	OGWAD78TV	CG320358	
C 402	17.6	62.9	712	5	BU279150	603862734	C 475	17.6	62.9	938	9	CG320358	OGWAD78TV	CG320358	
C 403	17.6	62.9	714	2	AW604480	RC3-C7025	476	17.6	62.9	940	4	EG328959	602428607	EG328959	
C 404	17.6	62.9	716	4	BM783695	K-EST0061	C 477	17.6	62.9	940	7	CN023543	AGENCOURT	CN023543	
C 405	17.6	62.9	718	7	CN297009	170005325	C 478	17.6	62.9	940	9	AG381101	Mus muscu	AG381101	
C 406	17.6	62.9	719	4	BG028676	602292843	C 479	17.6	62.9	947	9	CNS01UGA	Tetraodon	AL167773	
C 407	17.6	62.9	723	5	BX889819	BX889819	C 480	17.6	62.9	951	5	BQ880709	AGENCOURT	BQ880709	
C 408	17.6	62.9	725	2	BE741158	601593972	C 481	17.6	62.9	951	9	CG297953	OGK322TV	CG297953	
C 409	17.6	62.9	726	4	BG647192	EST508811	C 482	17.6	62.9	974	9	CC675627	OGK322TV	CC675627	
C 410	17.6	62.9	728	7	KA438166	GQ0082_TB	483	17.6	62.9	984	5	BU847463	AGENCOURT	BU847463	
C 411	17.6	62.9	736	1	AUI23805	AUI23805	484	17.6	62.9	1014	5	BX400988	BM454685	BM454685	
C 412	17.6	62.9	736	4	BG329293	602428369	485	17.6	62.9	1019	4	BM454685	AGENCOURT	BM454685	
C 413	17.6	62.9	737	7	CF765771	CES001184	C 486	17.6	62.9	1030	8	CC213267	CH261-115	CA487731	
C 414	17.6	62.9	737	8	BH330542	CH230-94F	C 487	17.6	62.9	1031	6	CA487731	AGENCOURT	CA487731	
C 415	17.6	62.9	743	8	CC091505	CSU-K33r	C 488	17.6	62.9	1052	9	CG389780	ZMMBGC057	CG389780	
C 416	17.6	62.9	745	9	AG611216	Mus muscu	C 489	17.6	62.9	1055	8	CC259342	CH261-164	CC259342	
C 417	17.6	62.9	747	4	BG445247	GA_EA002	C 490	17.6	62.9	1095	4	BM458217	AGENCOURT	BM458217	
C 418	17.6	62.9	749	1	AJ514223	AJ514223	491	17.6	62.9	1160	8	CC298015	CH261-66C	CC298015	
C 419	17.6	62.9	756	4	BM009562	603630130	492	17.6	62.9	1163	4	BG617997	602644871	BG617997	
C 420	17.6	62.9	756	5	BM943681	UI-M-EHOP	493	17.6	62.9	1188	8	CC230053	CH261-162	CC230053	
C 421	17.6	62.9	759	6	CD783348	EST654709	494	17.6	62.9	1280	9	CG749913	P044-2-CO	CG749913	
C 422	17.6	62.9	760	7	CF348492	AGENCOURT	C 495	17.6	62.9	1464	9	AG456367	Mus muscu	AG456367	
C 423	17.6	62.9	762	5	B0282598	603600412	C 496	17.6	62.9	1892	3	AK035824	Mus muscu	AK035824	
C 424	17.6	62.9	776	9	CL425240	ZMMBB043	C 497	17.6	62.9	2019	3	BC039779	Mus muscu	BC039779	
C 425	17.6	62.9	781	7	CO879294	BovGen.07	C 498	17.6	62.9	2082	3	BC024795	Mus muscu	BC024795	
C 426	17.6	62.9	782	4	B1970761	GM830011B	C 499	17.4	62.1	155	2	BF411513	UI-R-BT1-	BF411513	
C 427	17.6	62.9	784	6	CD655830	AGENCOURT	500	17.4	62.1	170	1	AU307722	AU307722	AU307722	
C 428	17.6	62.9	784	7	CF997918	AGENCOURT									
C 429	17.6	62.9	785	2	BE377560	601229748									
C 430	17.6	62.9	788	5	BP737773	BP737773									
C 431	17.6	62.9	794	9	CL768358	OR_BBA014									
C 432	17.6	62.9	798	9	CC599602	ZMMBGC040									
C 433	17.6	62.9	807	5	BU750277	CH3#032_B									
C 434	17.6	62.9	807	7	CK000763	AGENCOURT									
C 435	17.6	62.9	808	2	BE796639	601592035									
C 436	17.6	62.9	810	7	CF875234	tricc008xc									
C 437	17.6	62.9	811	6	CA386663	668305_NC									
C 438	17.6	62.9	816	1	AUI25141	AUI25141									
C 439	17.6	62.9	823	4	BI456132	603172791									
C 440	17.6	62.9	824	9	CR819111	GR0AA47B									
C 441	17.6	62.9	825	6	CA322414	UI-M-PXO-									
C 442	17.6	62.9	828	1	AUI140324	AUI140324									
C 443	17.6	62.9	829	5	BP171468	BP171468									
C 444	17.6	62.9	829	5	BQ042702	UI-M-EMO-									
C 445	17.6	62.9	833	7	CN330519	AGENCOURT									
C 446	17.6	62.9	835	7	CO248253	AGENCOURT									
C 447	17.6	62.9	837	9	CR109576	Reverse B									
C 448	17.6	62.9	837	9	CG360275	OG1BE17TV									
C 449	17.6	62.9	838	8	B2179405	CH230-444									
C 450	17.6	62.9	842	4	BG742315	602631215									
C 451	17.6	62.9	843	7	CO247163	AGENCOURT									
C 452	17.6	62.9	846	9	CG930556	ZMWBBC054									
C 453	17.6	62.9	848	6	CB245315	UI-M-FY0-									
C 454	17.6	62.9	851	4	B1101548	602887347									
C 455	17.6	62.9	855	9	CG052027	PUIIZ59TD									
C 456	17.6	62.9	857	8	B2265404	CH230-375									
C 457	17.6	62.9	862	5	B2379174	601238157									
C 458	17.6	62.9	865	2	CG360262	OG1BE17TH									
C 459	17.6	62.9	872	9	CG360262	OG1BE17TH									
C 460	17.6	62.9	875	2	BF530467	602071702									
C 461	17.6	62.9	883	6	CA791310	AGENCOURT									
C 462	17.6	62.9	887	5	BQ669108	AGENCOURT									
C 463	17.6	62.9	889	5	BQ922802	AGENCOURT									

AG407066	Mus musculus molossinus	DNA	linear	GSS 03-JUN-2004
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7,	genomic survey sequence.
AG407066	Mus musculus			

ALIGNMENTS

RESULT 1	AG407066	1040 bp	DNA	linear	GSS 03-JUN-2004
LOCUS	AG407066				
DEFINITION	Mus musculus molossinus DNA, clone:MSMg01-265P04.T7, genomic survey sequence.				
ACCESSION	AG407066				
VERSION	AG407066.1				GI:48049752
KEYWORDS	GSS.				
SOURCE	Mus musculus molossinus				
ORGANISM	Mus musculus molossinus				
REFERENCE	1				Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki Y.
AUTHORS	BAC and Sequences of Library MSMg01				
TITLE	Unpublished				
REFERENCE	2 (bases 1 to 1040)				Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki Y.
AUTHORS	Direct Submission				
TITLE	Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (s-matti@atc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/), Tel: 81-45-503-9111, Fax: 81-45-503-9170				
JOURNAL	Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199				

e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. .1040

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMG01-265P04.T7"

/sex="male"

/tissue_type="mixture of kidney and spleen"

/clone_lib="MSMG01 Mouse Male BAC Library"

ORIGIN

Query Match 70.7%; Score 19.8; DB 9; Length 476;
Best Local Similarity 80.8%; Pred. No. 6.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTT 26

DB 326 CCATCTCTCTCTTACCCCTGCTGTT 301

ORIGIN

Query Match 72.9%; Score 20.4; DB 9; Length 1040;
Best Local Similarity 84.0%; Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CATCTCTCANNATCCCTGCTGTTG 27

DB 648 CTCTCTCTCAACATCCCTGCTGTTG 672

RESULT 2

LOCUS

DEFINITION RPCI44_263K5.f RPCI-44 Sus scrofa genomic clone RPCI44_263K5,

genomic survey sequence.

CL336324 476 bp DNA linear GSS 19-AUG-2004

CL336324 1 GI:51388292

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 476)

Roqatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,

Beever,J.E. and Schook,L.B.

Piggy-BACing the Human Genome: Constructing a Porcine Physical Map

Through Comparative Genomics

Unpublished (2004)

Other GSSs: RPCI44_263K5.r

Contact: Lawrence B. Schook

Department of Animal Sciences

University of Illinois at Urbana Champaign

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 265 5326

Fax: 217 244 5617

Email: schook@uiuc.edu

Clones are derived from the porcine BAC library RPCI-44

(http://www.bacpac.chori.org/porcine242.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@chori.org).

Clones may be purchased from BACPAC Resources

(http://BACPACorders.chori.org). This work was undertaken as part

of the International Swine Genome Sequencing Consortium by

University of Illinois at Urbana Champaign, USA with funds provided

by grant No. AG2002-34480-11828 from USDA-CSREES and

AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing

Initiative)

Plate: 263 row: K column: 5

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .476

/organism="Sus scrofa"

/mol_type="genomic DNA"

/strain="four pigs (breed: 37.5% Yorks Landrace and 25%

Meishan)"

FEATURES

source

FEATURES

source

1. .287

Location/Qualifiers

1. .287

Location/Qualifiers

1. .287

Location/Qualifiers

1. .287

/db_xref="taxon:9823"

/clone="RPCI44_263K5"

/sex="male"

/cell_type="blood"

/clone_lib="RPCI-44"

/note="Vector: pTARBAC2; Site 1: EcoRI; Site 2: EcoRI;

porcine male BAC library produced by Pieter de Jong"

ORIGIN

Query Match 70.7%; Score 19.8; DB 9; Length 476;
Best Local Similarity 80.8%; Pred. No. 6.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTT 26

DB 326 CCATCTCTCTCTTACCCCTGCTGTT 301

RESULT 3

LOCUS

DEFINITION

BB338318 RIKEN full-length enriched, 10 days neonate cerebellum Mus

musculus cDNA clone B930012N10 3' similar to U13152 Mesocricetus

auratus guanine nucleotide-binding protein beta 5 (Gnbs) mRNA, mRNA

sequence.

BB338318 287 bp mRNA linear EST 11-JUL-2000

BB338318 1 GI:9047081

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 287)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,

Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,

Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,

Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,

Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,

Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,

Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,

Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,

Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,

Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,

Yokota,Y., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and

Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S.,

Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermostabilization of thermolabile enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Osawa,Y., Muramatsu,M.,

Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for

further details.

Location/Qualifiers

1. .287

Location/Qualifiers

1. .287

Location/Qualifiers

1. .287

Location/Qualifiers

1. .287

colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 58.6%; Score 19.2; DB 5; Length 481;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTG 27
DB 401 CCCACTTCCACGATCCCGAGCTGTG 427

RESULT 6

CN675425/c 511 bp mRNA linear EST 17-MAY-2004
LOCUS A0963B06-5 NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:A0963B06
IMAGE:30772817 5', mRNA sequence.

ACCESSION CN675425.1 GI:47441876
VERSION EST.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 511)
Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Falco,G., Martin,P.R., Staggs,C.A., Bassey,U.C., Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L., Schllessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A., Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A., D'Urso,M., Kelsio,J., Hide,W. and KO,M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLoS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula

TITLE

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0963 row: B column: 06
Seq primer: M13 Reverse
High quality sequence stop: 511
POLYA-No.

FEATURES

source Location/Qualifiers
1..511
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/EvTac"
/db_xref="niaEST:A0963B06-5"
/db_xref="taxon:10090"
/clone="NIA:A0963B06 IMAGE:30772817"
/sex="Male"
/tissue_type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long)"
/note="vector: pcMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES cells were plated at density 3x104/cm2, on gelatin-coated plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,

0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 1000 U/ml IIF, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGCGCGCCCTTTT-3'] from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pcMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.7 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 68.6%; Score 19.2; DB 7; Length 511;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTG 27
DB 234 CCCAGCTCATCAGATCCCTGCATTG 208

RESULT 7

LOCUS CC690447 577 bp DNA linear GSS 19-JUN-2003
DEFINITION OGXAB64TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0482K08, genomic survey sequence.

ACCESSION CC690447

VERSION CC690447.1 GI:32095223

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 577)
Whiteclaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

TITLE

Consortium for Maize Genomics

JOURNAL

Unpublished (2002)

COMMENT

Other GSSs: OGXAB64TV
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES

source Location/Qualifiers
1..577
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0482K08"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Query Match 68.6%; Score 19.2; DB 9; Length 577;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy 2 CCATCTCNCANNATCCCTGCTGTGG 28
Db 146 CCTGCTGTCAGCATCCCTGCAGTGG 172

RESULT 8
CD443887 646 bp mRNA linear EST 03-JUN-2003
DEFINITION EL01N0432D03.b Endosperm_4 Zea mays cDNA, mRNA sequence.
ACCESSION CD443887
VERSION CD443887.1 GI:31359530
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 646)
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
Larkins, B., Beckett, P. and Messing, J.
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Freelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakaman.rutgers.edu
Seq primer: T3.
FEATURES
source
Location/Qualifiers
1..646
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm 4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 68.6%; Score 19.2; DB 6; Length 646;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 276 CCGATGTCATCATTCATCCCGCTGTG 302

RESULT 9
AG063981/c
LOCUS AG063981
DEFINITION Pan troglodytes DNA, clone: PTB-052019.F, genomic survey sequence.
ACCESSION AG063981
VERSION AG063981.1 GI:16615783
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
2 (bases 1 to 659)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 626 CCCACCTCCACAGCATCCCGCTGTG 600

RESULT 10
AG291906/c
LOCUS AG291906
DEFINITION Mus musculus molossinus DNA, clone: MSMg01-067B08.TJ, genomic survey
sequence.
ACCESSION AG291906
VERSION AG291906.1 GI:47864860
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
2 (bases 1 to 681)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Teakuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Teakuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
source
Location/Qualifiers
1..659
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-052019.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 68.6%; Score 19.2; DB 9; Length 659;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 626 CCCACCTCCACAGCATCCCGCTGTG 600

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
source
Location/Qualifiers
1..659
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-052019.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 68.6%; Score 19.2; DB 9; Length 659;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 626 CCCACCTCCACAGCATCCCGCTGTG 600

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Teakuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Teakuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
source
Location/Qualifiers
1..681
/organism="Mus musculus molossinus"

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/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

Query Match      68.6%; Score 19.2; DB 9; Length 681;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CCATCTCTCCTGATCCCGGTGTGG 28
Db  153 CCATCTCTCCTGATCCCGGTGTGG 127

RESULT 11
AG345215/c
LOCUS      AG345215
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-139P01.TJ, genomic survey
sequence.
ACCESSION  AG345215
VERSION    AG345215.1 GI:47918525
KEYWORDS   GSS.
SOURCE     Mus musculus molossinus
ORGANISM   Mus musculus molossinus
REFERENCE  1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
AUTHORS    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE      BAC end Sequences of Library MSMg01
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 740)
AUTHORS    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT    Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@c.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector      : pBACe3.6
R.Site 1    : EcoRI
R.Site 2    : EcoRI.
FEATURES
source
location/Qualifiers
1..740
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

Query Match      68.6%; Score 19.2; DB 9; Length 740;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CCATCTCTCCTGATCCCGGTGTGG 28
Db  153 CCATCTCTCCTGATCCCGGTGTGG 127

RESULT 12
CL980943
LOCUS      CL980943
DEFINITION Oryza sativa indica cultivar-group)
ORIGIN
ACCESSION  CL980943
VERSION    CL980943.1 GI:52416373
KEYWORDS   GSS.
SOURCE     Oryza sativa (indica cultivar-group)
ORGANISM   Oryza sativa (indica cultivar-group)
REFERENCE  1 Oryza sativa (indica cultivar-group)
AUTHORS    Oryza sativa (indica cultivar-group)
TITLE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
JOURNAL    1 (bases 1 to 936)
COMMENT    Ma,L., Wang,C., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
location/Qualifiers
1..936
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/notes="Oryza sativa exon trapped genomic sequences"

Query Match      68.6%; Score 19.2; DB 9; Length 936;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CCATCTCTCCTGATCCCGGTGTGG 28
Db  157 CCATCTCTCCTGATCCCGGTGTGG 183

RESULT 13
CG232800
LOCUS      CG232800
DEFINITION Zea mays
ORIGIN
ACCESSION  CG232800
VERSION    CG232800.1 GI:34132686
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
REFERENCE  1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
AUTHORS    1 (bases 1 to 938)
TITLE      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Rasnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG2B120TH
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

```

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES

Location/Qualifiers
1..938
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0752D15"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 68.6%; Score 19.2; DB 9; Length 938;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCATCTCCTCANNATCCCTGCTGTGG 28
Db 51 CCTGCTCGTCAGCATCCCTGCAGTTGG 77

RESULT 14

CG456461/c
LOCUS 952 bp DNA linear GSS 17-SEP-2003
DEFINITION FUIJW63TDB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA0600K05,
genomic survey sequence.

ACCESSION CG456461
VERSION CG456461.1 GI:34841461
KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 952)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

AUTHORS

Maize Genomics Consortium

Unpublished (2003)

Other_GSSs: FUIJW63TDB

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

FEATURES

Location/Qualifiers
1..952
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0600K05"
/clone_lib="ZM 0.6 1.0 KB"
/note="Vector: pCF4-toPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"

ORIGIN

Query Match 68.6%; Score 19.2; DB 9; Length 952;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCATCTCCTCANNATCCCTGCTGTGG 28
Db 895 CCTGCTCGTCAGCATCCCTGCAGTTGG 869

RESULT 15

CNS06EAJ/c
LOCUS 961 bp DNA linear GSS 17-JUN-2001

DEFINITION T3 end of clone AR0AA020A08 of library AR0AA from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL394865

VERSION AL394865.1 GI:12146083

KEYWORDS GSS.

SOURCE

ORGANISM Zygosaccharomyces rouxii

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.

REFERENCE

1 (bases 1 to 961)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Boloitin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuvéglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekai, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissensbach, J.

AUTHORS

Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

FEBS Lett. 487 (1), 3-12 (2000)

20584711

11152876

2 (bases 1 to 961)

de Montigny, J., Straub, M., Potier, S., Tekai, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Souciet, J.

Genomic exploration of the hemiascomycetous yeasts: 8.

Zygosaccharomycetes rouxii

FEBS Lett. 487 (1), 52-55 (2000)

20584718

11152883

3 (bases 1 to 961)

Genoscope.

Direct Submission

Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomycetes
exiguus, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES

Location/Qualifiers
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/organism="Zygosaccharomycetes rouxii"
/mol_type="genomic DNA"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0AA020A08"
/clone_lib="AR0AA"
/note="end : T3"

misc_feature

<3..>419
/note="similar to Saccharomycetes cerevisiae ORF YNL289w [
PCU1 : cyclin, GI/S-specific]"
/evidence=not_experimental

ORIGIN

source

Query Match

Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy

1 CCATCTCCTCANNATCCCTGCTGTGG 27

Db

431 CCTAGCTCATTAGTATCCCTGCTGTGG 405

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RESULT 16
CG456420      1018 bp  DNA      linear  GSS 17-SEP-2003
LOCUS        PUIJW63TBB ZM 0.6-1.0 kb Zea mays genomic clone ZM600K05,
DEFINITION   genomic survey sequence.
ACCESSION    CG456420
VERSION      CG456420.1 GI:34841420
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 1018)
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
              Bennetzen,J.
TITLE        Maize Genomics Consortium
JOURNAL      Unpublished (2003)
COMMENT      Other GSSs: PUIJW63TDB
              Contact: Cathy Whitelaw
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: TR
              Class: sheared ends.
FEATURES     Location/Qualifiers
              1..1018
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /strain="B73"
               /db_xref="taxon:4577"
               /clone="ZM600K05"
               /clone_lib="ZM 0.6-1.0 kb"
               /notes="vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
               COT selected genomic DNA library"
ORIGIN
Query Match      68.6%; Score 19.2; DB 9; Length 1018;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2  CCATCTCTCANNATCCCTGCTGTGG 28
    |||||
Db   603 CCTGCTGTCAGCATCCCTGCGTTGG 629

RESULT 17
CG187707      1139 bp  DNA      linear  GSS 08-MAY-2003
LOCUS        CH261-33N7 Sp6.1 CH261 Gallus gallus genomic clone CH261-33N7,
DEFINITION   genomic survey sequence.
ACCESSION    CG187707
VERSION      CG187707.1 GI:30431607
KEYWORDS     GSS.
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 1139)
AUTHORS      Warren,W., Graves,T., Nardis,E. and Wilson,R.
              Gallus gallus BAC End Reads
              Unpublished (2003)
              Contact: Richard K. Wilson
              Genome Sequencing Center
              Washington University School of Medicine
              Email: submissions@watson.wustl.edu
              Insert Length: 182000 Std Error: 0.00

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Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 145
High quality sequence stop: 618.
Location/Qualifiers
1..1139
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-33N7"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /notes="vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"

```

FEATURES

source

ORIGIN

```

Query Match      68.6%; Score 19.2; DB 8; Length 1139;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2  CCATCTCTCANNATCCCTGCTGTGG 28
    |||||
Db   131 CCAGCTCATCTATATCCTGCTGTGG 157

```

RESULT 18

BC026893/c

LOCUS

BC026893

2314 bp

linear

HTC 19-NOV-2003

DEFINITION

Mus musculus downstream of Stkl, mRNA (cdna clone IMAGE:3982045),

with apparent retained intron.

ACCESSION

BC026893

VERSION

BC026893.1

GI:22268016

KEYWORDS

HTC.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 2314)

AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zengberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heideh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Cheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullany,S.J., Bosak,S.A., McSwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,

Schneerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2314)

Strausberg,R.

Direct Submission

Submitted (04-APR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

REMARK

COMMENT

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IPAK Plate: 40 Row: i Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis
 This clone has the following problem: retained intron.

FEATURES

Location/Qualifiers
 1..2314
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:3982045"
 /tissue_type="Mammary tumor metastasized to lung. Tumor
 arose spontaneously from a senescent normal mammary
 (clonal) outgrowth infected with the virus MMTV."
 /clone_lib="NCI CGAP_Lu29"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 68.6%; Score 19.2; DB 3; Length 2314;
 Best Local Similarity 77.8%; Pred. No. 1.6e+03;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CCCATCTCCTCCTCCTCCTGTTG 27
 ||||| ||||| ||||| ||||| |||||
 Db 1769 CCAATCTCGTCATCTCCTCCTGAGTTG 1743

RESULT 19

BF723268/c
 LOCUS
 DEFINITION
 mab30401.y1 Soares NMEBA branchial_arch Mus musculus cDNA clone
 IMAGE:3971616 5' similar to TR:Q9Y3V6 Q9Y3V6 HYPOTHETICAL 22.9 KD
 PROTEIN ;, mRNA sequence.

ACCESSION

BF723268
 VERSION
 KEYWORDS
 SOURCE

BF723268.1 GI:12024270
 EST.
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (Bases 1 to 413)
 AUTHORS
 TITLE
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

COMMENT
 Other ESTs: mab30a01.x1
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1471648

Seq primer: -40RP from Gibco
 High quality sequence stop: 401.

FEATURES

Location/Qualifiers
 1..413
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:3971616"
 /tissue_type="branchial arches"
 /dev_stage="embryo, 10.5 dpc"
 /lab_host="DH10B (phage resistant)"
 /clone_lib="Soares NMEBA branchial_arch"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTACCAATCTGAGTGGAGCGCGCATGATTTTTTTTTTTTTTTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT7T3 vector. Library
 constructed and normalized by Bento Soares and M.Fatima
 Bonaldo."

ORIGIN

Query Match 67.1%; Score 18.8; DB 2; Length 413;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CCATCTCCTCANNATCCCTGCTGT 25
 ||||| ||||| ||||| ||||| |||||
 Db 34 CCCATCTCCTCATAATCTCTGCTCT 10

RESULT 20

CF546284/c
 LOCUS
 DEFINITION

lae70c10.y1 Gastric Epithelial Progenitor Mus musculus cDNA 5'
 similar to SW:PRCF HUMAN P40306 PROTEASOME COMPONENT MECL-1
 PRECURSOR ;, mRNA sequence.

ACCESSION

CF546284
 VERSION
 KEYWORDS
 SOURCE

ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (Bases 1 to 445)
 AUTHORS
 TITLE
 WashU Stem cell EST Project
 Unpublished (2002)
 Contact: Jeff Gordon and Mike Lovett
 WashU, Human Genetics Division
 Washington University School of Medicine
 1st strand of cDNA was synthesized with reverse transcriptase and
 oligo(dT) beads, then cDNA was amplified by PCR using modified
 SMART primers. The final cDNA was cloned in pAMP1 vector in
 annealing reaction with Uracil DNA Glycosylase (UDG). Library
 constructed by Y.Korshunova and M. Lovett. Library materials
 provided by Mills JC & Gordon JI.
 Seq primer: -40RP from Gibco

JOURNAL

COMMENT
 High quality sequence stop: 445.

Location/Qualifiers
 1..445

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/tissue_type="Gastric Epithelial Progenitor"

/dev_stage="adult"

/lab_host="DH5alpha"

/clone_lib="Gastric Epithelial Progenitor"

TITLE
JOURNAL

REFERENCE
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
2 (bases 1 to 990)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissensbach,J.
AUTHORS
Direct Submission
TITLE
JOURNAL

COMMENT
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
source
1. .990
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="18E03"
/clone_lib="NotreDame1"
/note="end : SP6"

ORIGIN
Query Match 67.1%; Score 18.8; DB 9; Length 990;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 525 CCCATCTCGTCTTTGTCCTGCTGT 501

RESULT 24
CLO25440/c
LOCUS
DEFINITION
CH216-21K12.RM1.1 CH216 Xenopus tropicalis genomic clone
CH216-21K12, genomic survey sequence.
ACCESSION
CLO25440
VERSION
CLO25440.1 GI:40468154
KEYWORDS
GSS.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 1137)
AUTHORS
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
TITLE
JOURNAL
COMMENT
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGAGGA
Class: BAC ends
High quality sequence start: 100
High quality sequence stop: 743.
Location/Qualifiers
1. .1137
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-21K12"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

FEATURES
source
1. .1137
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-21K12"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN
Query Match 67.1%; Score 18.8; DB 9; Length 1137;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 CATCTCNCANNATCCCTGCTGTG 27
Db 596 CACCTCTCTTTATCCCTGCTGTG 572

RESULT 25
CG755418/c
LOCUS
DEFINITION
P051-1-C06.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
ACCESSION
CG755418
VERSION
CG755418.1 GI:37981893
KEYWORDS
GSS.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 2185)
AUTHORS
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE
JOURNAL
COMMENT
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE
22835951
PUBMED
12884007
CONTACT: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
1. .2185
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match 67.1%; Score 18.8; DB 9; Length 2185;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1447 CCCATCAGCTCAGGATCCCTGCTAT 1423

RESULT 26
BF655438
LOCUS
DEFINITION
279922 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
BF655438
VERSION
BF655438.1 GI:11920555
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 231)
AUTHORS
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 11282978
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGTCACGACG
 Plate: 76 row: J column: 7
 Seq primer: ATTAGTGACACTATAG.
 Location/Qualifiers
 1..231
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH108"
 /clone_lib="MARC 3BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
 ORIGIN
 Query Match 66.4%; Score 18.6; DB 2; Length 231;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CCCATCTCTCANNATCCCTCGCTGTGG 28
 |||||
 Db 27 CCTGCTCTTCACCTTCGCTGTGG 54
 RESULT 27
 BF655439
 LOCUS 279923 MARC 3BOV Bos taurus cDNA 5', mRNA sequence. EST 25-APR-2001
 DEFINITION
 ACCESSION BF655439
 VERSION BF655439.1 GI:11920556
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 231)
 Smith, T.P.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 11282978
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366

Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGTCACGACG
 Plate: 76 row: J column: 8
 Seq primer: ATTAGTGACACTATAG.
 Location/Qualifiers
 1..231
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH108"
 /clone_lib="MARC 3BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
 ORIGIN
 Query Match 66.4%; Score 18.6; DB 2; Length 231;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CCCATCTCTCANNATCCCTCGCTGTGG 28
 |||||
 Db 27 CCTGCTCTTCACCTTCGCTGTGG 54
 RESULT 28
 AV361516/c
 LOCUS AV361516 RIKEN full-length enriched, adult male eyeball Mus musculus cDNA clone 7530428D08 3' similar to D29639 Mouse embryonal carcinoma cell mRNA for 3-hydroxyacyl CoA dehydrogenase, mRNA sequence.
 ACCESSION AV361516
 VERSION AV361516.1 GI:6408804
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 239)
 Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tomnaga, N., Tsunoda, Y., Watahiki, A., Yamabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Konno, H., et al. 1999)
 Unpublished (1999)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)


```

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIONP462H01375"
/lab_host="DH10B"
/clone_lib="pBluescript Lion"

ORIGIN
Query Match      66.4%; Score 18.6; DB 5; Length 245;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
    |||||
Db 105 CCTGCTCTTCACCTTCGCTGTGTGG 78

RESULT 32
AW354424
LOCUS      280 bp mRNA linear EST 25-APR-2001
DEFINITION 36211 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  AW354424
VERSION     AW354424.1 GI:6853414
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.

REFERENCE 1 (bases 1 to 280)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keefe,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)

TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle

JOURNAL   MEDLINE
PUBMED    11180013
COMMENT   Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACACGCTATGACCAT
            BACKWARD: GTTTCACGATCAGCAGC
            Plate: 23 row: 0 column: 11
            Seq primer: ATTTAGTGACACTATAG.

FEATURES             Location/Qualifiers
     source           1..280
     organism="Bos taurus"
     mol_type="mRNA"
     db_xref="taxon:9913"
     tissue_type="pooled"
     /lab_host="DH10B"
     /clone_lib="MARC 1BOV"
     /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
     Library made from pooled tissue from lymph node, ovary,
     fat, hypothalamus, and pituitary."

ORIGIN
Query Match      66.4%; Score 18.6; DB 2; Length 280;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
    |||||
Db 112 CCTGCTCTTCACCTTCGCTGTGTGG 139

RESULT 33
AV116369
LOCUS      285 bp mRNA linear EST 30-JUN-1999
DEFINITION  AV116369 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA
            clone 2610105H23, mRNA sequence.
ACCESSION  AV116369
VERSION     AV116369.1 GI:5298520
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIONP462H01375"
/lab_host="DH10B"
/clone_lib="pBluescript Lion"

ORIGIN
Query Match      66.4%; Score 18.6; DB 5; Length 245;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
    |||||
Db 105 CCTGCTCTTCACCTTCGCTGTGTGG 78

RESULT 32
BF440266/c
LOCUS      274 bp mRNA linear EST 01-DEC-2000
DEFINITION  B529000208903 Lewin Cattle Spleen Bos taurus cDNA clone
            B529000208903 3', mRNA sequence.
ACCESSION  BF440266
VERSION     BF440266.1 GI:11500149
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.

REFERENCE 1 (bases 1 to 274)
AUTHORS   Band,M.R., Larson,J.H., Rebeiz,M., Green,C.A., Heyen,D.W.,
            Donovan,J., Windish,R., Steining,C., Mahyuddin,P., Womack,J. and
            Lewin,H.A.
            An ordered comparative map of the cattle and human genomes
            Genome Res. 10 (9), 1359-1368 (2000)

TITLE     An ordered comparative map of the cattle and human genomes

JOURNAL   MEDLINE
PUBMED    10984454
COMMENT   Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Funding for Cattle EST sequencing was provided by the USDA National
            Research Initiative, Project No. 98-35205-6644, and a grant from
            the Japanese Ministry of Agriculture Fisheries and Forestry to
            H.A.Lewin and J.E.Womack. Base-calling/Quality scores: PHRED or
            Washington University Genome Center.Vector-trimming: Cross Match
            from Washington University Genome Center PHRAP suite. This sequence
            is vector free and at least 150bp in length.
            Insert Length: 274 Std Error: 0.00
            Seq primer: TAGACTCATTAGGCGGAT
            High quality sequence stop: 274.

FEATURES             Location/Qualifiers
     source           1..274
     organism="Bos taurus"
     mol_type="mRNA"
     strain="Angus"
     /db_xref="taxon:9913"
     /clone="B529000208903"
     /sex="Female"
     /dev stage="Adult"
     /clone_lib="Lewin Cattle Spleen"
     /note="Organ: Spleen; Vector: pBluescript SK(+/-)"

ORIGIN
Query Match      66.4%; Score 18.6; DB 2; Length 274;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
    |||||
Db 36 CCCACTCTCTACTCTCCCTGCTGTGG 63

```



```

/tissue_types="Blood"
/cell_type="myeloma"
/dev_stage="multiple myeloma"
/clone_lib="Myeloma (MVE) cDNA library"
/notes="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2: XhoI; Myeloma cells from multiple myeloma patients' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MLV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and [a-32P]dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x106. Clones from the primary library were randomly selected for single pass sequencing."
ORIGIN
Query Match 66.4%; Score 18.6; DB 2; Length 300;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CCATCTCTTCANNATCCCTGCTGTGG 28
||||| ||| |||||
DB 166 CCATCTCTGCACAGCCGTGCTGTGG 139
RESULT 36
CR405165 315 bp DNA linear GSS 02-MAY-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-876C05-026468,
DEFINITION genomic survey sequence.
ACCESSION CR405165
VERSION CR405165.1 GI:46945893
KEYWORDS GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosids; eustosida II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weisshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4
AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
TITLE Direct Submission

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JOURNAL

COMMENT

Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone T2219. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source	Location/Qualifiers
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	/clone="GK-876C05-026468"
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	/ecotype="Col-0"
	/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match	66.4%; Score 18.6; DB 9; Length 315;
Best Local Similarity	75.0%; Pred. No. 2.2e+03;
Matches	21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY

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1 CCATCTCTCNATTCCATCCCTGCTGTGG 28
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5 CCAATTTCTACATTATCCCTGCTGTGG 32

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DB

RESULT 37

C0727823/c

LOCUS

DEFINITION

UMC-bend_0A02-024-d02 Day 16 Uterus from a pregnant animal bend Bos taurus cDNA 3', mRNA sequence.

ACCESSION

C0727823

VERSION

C0727823.1 GI:50710853

KEYWORDS

EST.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 348)
Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C., Roberts,R.N., Smith,M.F. and Youngquist,R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female Reproduction Unpublished (2002)

AUTHORS

Contact: DNA Core Facility (Bovine Project)

TITLE

Animal Science - RS Prather

JOURNAL

University of Missouri-Columbia

COMMENT

M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: bovine@net.missouri.edu
POLYA=Yes.

FEATURES

source	Location/Qualifiers
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	/mol_type="mRNA"
	/db_xref="taxon:9913"
	/clone_lib="bend"
	/note="Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather,

E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlearanch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.mst.missouri.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)⁺ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the Superscript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, lmcg of poly(A)⁺ RNA was annealed at 37 degrees with 10mcg of NotI-tag-dt18 oligonucleotide (GCTGCTCGGCGGC-tag-T18) and reverse transcribed at 37 degrees with Superscript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uiowa.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and Rnase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SpOtk6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dt18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SpOtk6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails,

genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's Bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Sivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jelene, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG TISSUE=Day 16 Uterus from a pregnant animal TAG_SEQ=CAACGTGTG"

ORIGIN

Query Match 66.4%; Score 18.6; DB 7; Length 348;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTGG 28
DB 208 CCTGCTCTTCACTGCTGCTGCTGTGG 181

RESULT 38

BF601010 389 bp mRNA linear EST 25-APR-2001
LOCUS BF601010
DEFINITION B65865 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF601010
VERSION BF601010.1 GI:11698231
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 389)
Smith, T.P.L., Grosbe, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978

REFERENCE

AUTHORS
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 39 row: C column: 20

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Search completed: July 31, 2005, 13:47:43
Job time : 1747.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:23:11 ; Search time 71.5 Seconds
(without alignments)
640.780 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccatctctcannatccctgtctgtgg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA.*

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6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	21.8	77.9	3381	3	US-08-915-152-1
C 5	21.8	77.9	3381	3	US-08-915-152-2
C 6	21.8	77.9	3381	4	US-09-376-463-2
C 7	21.8	77.9	3381	5	PCT-US96-07627-1
C 8	21.8	77.9	3381	5	PCT-US96-07627-2
C 9	20.2	72.1	10718	3	US-08-325-426B-1
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C 11	18.8	67.1	5674	1	US-08-190-411A-1
C 12	18.8	67.1	5674	1	US-08-299-849B-8
C 13	18.8	67.1	5674	2	US-08-560-024-1
C 14	18.8	67.1	5674	2	US-08-142-368A-8
C 15	18.8	67.1	5674	3	US-08-967-727-8
C 16	18.8	67.1	5674	3	US-08-037-230D-8
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C 19	18.8	67.1	5674	4	US-09-404-026-8
C 20	18.8	67.1	5674	4	US-09-312-464-8
C 21	18.8	67.1	5699	4	US-09-949-016-12445
C 22	18.8	67.1	5699	4	US-09-949-016-14430
C 23	18.8	67.1	5707	2	US-08-472-809B-8
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C 25	18.6	66.4	601	4	US-09-949-016-198635
C 26	18.6	66.4	767677	4	US-09-949-016-12147
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C 53	17.6	62.9	19025	4	US-10-697-266-3	Sequence 3, Appli
C 54	17.6	62.9	31960	3	US-09-453-702B-11	Sequence 11, Appl
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C 73	17	60.7	363	4	US-09-270-767-25021	Sequence 25021, A
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C 78	17	60.7	4629	2	US-08-150-811-7	GENERAL INFORMA
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C 81	17	60.7	4832	4	US-09-470-618-14	Sequence 14, Appl
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C 84	17	60.7	5035	2	US-08-558-107-1	Sequence 1, Appli
C 85	17	60.7	5035	2	US-09-243-539-1	Sequence 1, Appli
C 86	17	60.7	5035	3	US-09-949-016-16152	Sequence 16152, A
C 87	17	60.7	6883	4	US-08-276-594A-1	Sequence 1, Appli
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105	17	60.7	9080	4	US-09-001-039B-44	Sequence 44, Appli	C 178	57.9	601	4	US-09-949-016-40348	Sequence 40348, A
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107	17	60.7	9354	1	US-08-683-839B-2	Sequence 2, Appli	C 180	57.9	601	4	US-09-949-016-135034	Sequence 135034, A
108	17	60.7	11846	4	US-09-205-817A-4	Sequence 4, Appli	C 181	57.9	601	4	US-09-949-016-198748	Sequence 198748, A
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112	17	60.7	12394	3	US-09-488-856A-10	Sequence 10, Appli	C 185	57.9	601	4	US-09-949-016-198752	Sequence 198752, A
113	17	60.7	24070	4	US-09-949-016-16153	Sequence 16153, A	C 186	57.9	601	4	US-09-949-016-201613	Sequence 201613, A
C 114	17	60.7	26012	4	US-09-902-540-1212	Sequence 1212, Ap	C 187	57.9	1050	4	US-09-248-796A-3692	Sequence 3692, Ap
C 115	17	60.7	42325	4	US-08-311-731A-131	Sequence 131, App	C 188	57.9	2171	3	US-08-811-481-1	Sequence 1, Appli
C 116	17	60.7	44998	4	US-09-949-016-12824	Sequence 12824, A	C 189	57.9	2171	4	US-09-876-527-1	Sequence 1, Appli
C 117	17	60.7	44999	4	US-09-949-016-14832	Sequence 14832, A	C 190	57.9	2240	4	US-09-799-451-571	Sequence 571, App
C 118	17	60.7	44999	4	US-09-949-016-14833	Sequence 14833, A	C 191	57.9	2460	3	US-09-305-681-3	Sequence 3, Appli
C 119	17	60.7	44999	4	US-09-949-016-17108	Sequence 17108, A	C 192	57.9	2542	3	US-09-305-681-5	Sequence 5, Appli
C 120	17	60.7	44999	4	US-09-949-016-17109	Sequence 17109, A	C 193	57.9	2559	4	US-09-248-796A-787	Sequence 787, App
C 121	17	60.7	85675	4	US-09-949-016-12333	Sequence 12333, A	C 194	57.9	2736	3	US-08-811-481-23	Sequence 23, Appli
C 122	17	60.7	85675	4	US-09-949-016-12336	Sequence 12336, A	C 195	57.9	2736	4	US-09-876-527-23	Sequence 23, Appli
C 123	17	60.7	85210	4	US-09-949-016-16986	Sequence 16986, A	C 196	57.9	3287	3	US-08-811-481-15	Sequence 15, Appli
C 124	17	60.7	95109	4	US-09-949-016-16027	Sequence 16027, A	C 197	57.9	3287	4	US-09-876-527-15	Sequence 15, Appli
C 125	17	60.7	142783	4	US-09-949-016-15127	Sequence 15127, A	C 198	57.9	3330	3	US-09-550-338-1	Sequence 1, Appli
C 126	17	60.7	154600	4	US-09-949-016-14757	Sequence 14757, A	C 199	57.9	3390	4	US-09-767-878-1	Sequence 1, Appli
C 127	16.8	60.0	222	4	US-09-513-999C-27632	Sequence 27632, A	C 200	57.9	4609	4	US-09-919-039-340	Sequence 340, App
C 128	16.8	60.0	981	4	US-09-543-681A-2168	Sequence 2168, Ap	C 201	57.9	4855	4	US-09-876-594-847	Sequence 847, App
C 129	16.8	60.0	9480	4	US-09-657-013-35	Sequence 35, Appli	C 202	57.9	4876	4	US-09-949-016-12790	Sequence 12790, A
C 130	16.8	60.0	10087	4	US-09-657-013-29	Sequence 29, Appli	C 203	57.9	4877	4	US-09-949-016-14084	Sequence 14084, A
C 131	16.8	60.0	85122	4	US-09-949-016-14693	Sequence 14693, A	C 204	57.9	10701	4	US-09-949-016-14375	Sequence 14375, A
C 132	16.8	60.0	94077	4	US-09-949-016-13635	Sequence 13635, A	C 205	57.9	111235	4	US-09-949-016-15328	Sequence 15328, A
C 133	16.8	60.0	119214	4	US-09-949-016-12507	Sequence 12507, A	C 206	57.9	139150	4	US-09-949-016-17398	Sequence 17398, A
C 134	16.8	60.0	154600	4	US-09-949-016-14757	Sequence 14757, A	C 207	57.9	139577	4	US-09-949-016-12879	Sequence 12879, A
C 135	16.6	59.3	222	1	US-08-248-474-88	Sequence 88, Appli	C 208	57.9	163662	4	US-09-949-016-12545	Sequence 12545, A
C 136	16.6	59.3	222	3	US-08-756-849-88	Sequence 88, Appli	C 209	57.9	163664	4	US-09-949-016-13546	Sequence 13546, A
C 137	16.6	59.3	324	4	US-08-155-106-29	Sequence 29, Appli	C 210	57.9	165651	4	US-09-949-016-13032	Sequence 13032, A
C 138	16.6	59.3	394	4	US-09-513-999C-3611	Sequence 3611, Ap	C 211	57.9	194714	4	US-09-949-016-11869	Sequence 11869, A
C 139	16.6	59.3	456	4	US-09-621-976-400	Sequence 400, App	C 212	57.9	196714	4	US-09-949-016-15474	Sequence 15474, A
C 140	16.6	59.3	491	4	US-09-270-767-12530	Sequence 12530, A	C 213	57.9	221958	4	US-09-949-016-12173	Sequence 12173, A
C 141	16.6	59.3	601	4	US-09-949-016-60003	Sequence 60003, A	C 214	57.9	221966	4	US-09-949-016-15498	Sequence 15498, A
C 142	16.6	59.3	601	4	US-09-949-016-69043	Sequence 69043, A	C 215	57.9	256171	4	US-09-949-016-12822	Sequence 12822, A
C 143	16.6	59.3	1106	1	US-08-389-668A-3	Sequence 3, Appli	C 216	57.9	256176	4	US-09-949-016-15524	Sequence 15524, A
C 144	16.6	59.3	1106	1	US-08-732-506-3	Sequence 3, Appli	C 217	57.9	276	2	US-08-273-146-46	Sequence 46, Appli
C 145	16.6	59.3	1106	5	PCT-US95-05768-3	Sequence 3, Appli	C 218	57.9	321	2	US-08-672-176A-2	Sequence 2, Appli
C 146	16.6	59.3	1295	3	US-08-806-263-1	Sequence 1, Appli	C 219	57.9	341	4	US-09-513-999C-17702	Sequence 17702, A
C 147	16.6	59.3	1764	4	US-09-799-451-602	Sequence 602, App	C 220	57.9	343	4	US-09-621-976-17847	Sequence 17847, A
C 148	16.6	59.3	2938	3	US-08-969-815-3	Sequence 3, Appli	C 221	57.9	447	2	US-08-579-940-1	Sequence 1, Appli
C 149	16.6	59.3	2938	3	US-09-120-025-3	Sequence 3, Appli	C 222	57.9	447	3	US-08-838-692-3	Sequence 3, Appli
C 150	16.6	59.3	2938	3	US-09-710-481-3	Sequence 3, Appli	C 223	57.9	489	4	US-09-621-976-2891	Sequence 2891, Ap
C 151	16.6	59.3	2938	4	US-09-553-875-3	Sequence 3, Appli	C 224	57.9	554	3	US-08-348-548-3	Sequence 3, Appli
C 152	16.6	59.3	2938	4	US-09-768-670-3	Sequence 3, Appli	C 225	57.9	554	5	PCT-US95-15716-3	Sequence 3, Appli
C 153	16.6	59.3	2938	4	US-09-796-286-3	Sequence 3, Appli	C 226	57.9	601	4	US-09-949-016-45560	Sequence 45560, A
C 154	16.6	59.3	3211	2	US-08-574-959A-8	Sequence 8, Appli	C 227	57.9	601	4	US-09-949-016-85912	Sequence 85912, A
C 155	16.6	59.3	3211	3	US-09-357-014-8	Sequence 8, Appli	C 228	57.9	601	4	US-09-949-016-85913	Sequence 85913, A
C 156	16.6	59.3	3225	4	US-09-799-451-238	Sequence 238, App	C 229	57.9	601	4	US-09-949-016-85914	Sequence 85914, A
C 157	16.6	59.3	3901	2	US-08-574-959A-6	Sequence 6, Appli	C 230	57.9	601	4	US-09-949-016-86476	Sequence 86476, A
C 158	16.6	59.3	3901	3	US-09-357-014-6	Sequence 6, Appli	C 231	57.9	601	4	US-09-949-016-192789	Sequence 192789, A
C 159	16.6	59.3	7409	4	US-09-949-016-12689	Sequence 12689, A	C 232	57.9	601	4	US-09-949-016-192790	Sequence 192790, A
C 160	16.6	59.3	7409	4	US-09-949-016-15978	Sequence 15978, A	C 233	57.9	601	4	US-09-949-016-198411	Sequence 198411, A
C 161	16.6	59.3	14485	4	US-09-876-216-3	Sequence 3, Appli	C 234	57.9	601	4	US-09-949-016-198412	Sequence 198412, A
C 162	16.6	59.3	24984	4	US-09-949-016-14950	Sequence 14950, A	C 235	57.9	601	4	US-09-949-016-198413	Sequence 198413, A
C 163	16.6	59.3	31166	4	US-09-949-016-13464	Sequence 13464, A	C 236	57.9	652	2	US-08-737-129A-7	Sequence 7, Appli
C 164	16.6	59.3	34363	4	US-09-949-016-16341	Sequence 16341, A	C 237	57.9	689	4	US-09-270-767-4849	Sequence 4849, Ap
C 165	16.6	59.3	86116	4	US-09-949-016-14766	Sequence 14766, A	C 238	57.9	689	4	US-09-270-767-20131	Sequence 20131, A
C 166	16.6	59.3	96866	4	US-09-949-016-13768	Sequence 13768, A	C 239	57.9	920	2	US-08-860-174A-3	Sequence 3, Appli
C 167	16.6	59.3	158735	4	US-09-949-016-11989	Sequence 11989, A	C 240	57.9	920	3	US-09-171-025-24	Sequence 24, Appli
C 168	16.6	59.3	158735	4	US-09-949-016-17130	Sequence 17130, A	C 241	57.9	920	4	US-09-742-693-28	Sequence 28, Appli
C 169	16.6	59.3	312474	4	US-09-949-016-17434	Sequence 17434, A	C 242	57.9	1017	4	US-09-902-540-7918	Sequence 7918, Ap
C 170	16.6	59.3	343352	4	US-09-949-016-13498	Sequence 13498, A	C 243	57.9	1120	3	US-08-851-190-4	Sequence 4, Appli
C 171	16.4	58.6	32958	4	US-09-949-016-15677	Sequence 15677, A	C 244	57.9	1494	4	US-09-302-540-8019	Sequence 8019, Ap
C 172	16.4	58.6	265038	4	US-09-949-016-15779	Sequence 15779, A	C 245	57.9	1692	3	US-09-421-017B-664	Sequence 664, App
C 173	16.2	57.9	440	4	US-09-621-976-11347	Sequence 11347, A	C 246	57.9	1706	2	US-08-860-174A-11	Sequence 11, Appli

C 247	16	57.1	1706	3	US-09-171-025-27	Sequence 27, Appl	C 320	15.8	56.4	44971	4	US-09-949-016-17049	Sequence 17049, A
C 248	16	57.1	1745	3	US-09-171-025-1	Sequence 1, Appl	C 321	15.8	56.4	46319	4	US-09-949-016-17526	Sequence 17526, A
C 249	16	57.1	1952	4	US-09-566-921-24	Sequence 24, Appl	C 322	15.8	56.4	46323	4	US-09-949-016-17526	Sequence 17526, A
C 250	16	57.1	2091	4	US-09-489-039A-5233	Sequence 5233, Ap	C 323	15.8	56.4	78125	4	US-09-949-016-16006	Sequence 16006, A
C 251	16	57.1	2154	3	US-09-488-856A-3	Sequence 3, Appl	C 324	15.8	56.4	99748	4	US-09-949-016-11990	Sequence 11990, A
C 252	16	57.1	2318	4	US-09-488-856A-3	Sequence 4687, Ap	C 325	15.8	56.4	99749	4	US-09-949-016-16518	Sequence 16518, A
C 253	16	57.1	2341	4	US-09-620-3120-423	Sequence 423, App	C 326	15.8	56.4	113538	4	US-09-949-016-16329	Sequence 16329, A
C 254	16	57.1	2343	2	US-09-031-392-1	Sequence 1, Appl	C 327	15.8	56.4	209210	4	US-09-949-016-15094	Sequence 15094, A
C 255	16	57.1	2343	3	US-09-299-549-1	Sequence 1, Appl	C 328	15.8	56.4	227390	4	US-09-949-016-12201	Sequence 12201, A
C 256	16	57.1	2343	3	US-09-610-417-1	Sequence 1, Appl	C 329	15.8	56.4	227391	4	US-09-949-016-13365	Sequence 13365, A
C 257	16	57.1	2968	4	US-09-949-016-131	Sequence 131, App	C 330	15.8	56.4	228896	4	US-09-949-016-17127	Sequence 17127, A
C 258	16	57.1	3455	4	US-10-009-332-31	Sequence 31, Appl	C 331	15.8	56.4	254405	4	US-09-949-016-14381	Sequence 14381, A
C 259	16	57.1	3462	4	US-10-009-332-30	Sequence 30, Appl	C 332	15.6	55.7	328	4	US-09-513-999C-3055	Sequence 3055, Ap
C 260	16	57.1	3464	4	US-10-009-332-26	Sequence 26, Appl	C 333	15.6	55.7	601	4	US-09-949-016-29682	Sequence 29682, A
C 261	16	57.1	3467	4	US-10-009-332-25	Sequence 25, Appl	C 334	15.6	55.7	601	4	US-09-949-016-29683	Sequence 29683, A
C 262	16	57.1	3467	4	US-10-009-332-29	Sequence 29, Appl	C 335	15.6	55.7	601	4	US-09-949-016-29825	Sequence 29825, A
C 263	16	57.1	3469	4	US-10-009-332-27	Sequence 27, Appl	C 336	15.6	55.7	601	4	US-09-949-016-29826	Sequence 29826, A
C 264	16	57.1	3470	4	US-10-009-332-28	Sequence 28, Appl	C 337	15.6	55.7	601	4	US-09-949-016-33606	Sequence 33606, A
C 265	16	57.1	3473	4	US-10-009-332-24	Sequence 24, Appl	C 338	15.6	55.7	601	4	US-09-949-016-63265	Sequence 63265, A
C 266	16	57.1	4149	4	US-09-799-451-820	Sequence 820, App	C 339	15.6	55.7	601	4	US-09-949-016-64735	Sequence 64735, A
C 267	16	57.1	5357	4	US-09-979-765-1	Sequence 21, Appl	C 340	15.6	55.7	601	4	US-09-949-016-147598	Sequence 147598, A
C 268	16	57.1	7825	4	US-09-949-016-14399	Sequence 14399, A	C 341	15.6	55.7	601	4	US-09-949-016-65547	Sequence 65547, A
C 269	16	57.1	8241	4	US-09-902-540-798	Sequence 798, App	C 342	15.6	55.7	601	4	US-09-949-016-87236	Sequence 87236, A
C 270	16	57.1	8285	3	US-09-732-025-3	Sequence 3, Appl	C 343	15.6	55.7	601	4	US-09-949-016-105170	Sequence 105170, A
C 271	16	57.1	9033	4	US-09-902-540-815	Sequence 815, App	C 344	15.6	55.7	601	4	US-09-949-016-131729	Sequence 131729, A
C 272	16	57.1	9723	1	US-08-083-590A-21	Sequence 21, Appl	C 345	15.6	55.7	601	4	US-09-949-016-137730	Sequence 137730, A
C 273	16	57.1	9723	3	US-08-532-384-21	Sequence 21, Appl	C 346	15.6	55.7	601	4	US-09-949-016-147598	Sequence 147598, A
C 274	16	57.1	11827	3	US-09-739-455-3	Sequence 3, Appl	C 347	15.6	55.7	601	4	US-09-949-016-17599	Sequence 17599, A
C 275	16	57.1	14967	4	US-09-949-016-15448	Sequence 15448, A	C 348	15.6	55.7	601	4	US-09-949-016-157435	Sequence 157435, A
C 276	16	57.1	15164	4	US-09-919-497-20	Sequence 20, Appl	C 349	15.6	55.7	601	4	US-09-949-016-157436	Sequence 157436, A
C 277	16	57.1	21721	4	US-09-269-939A-41	Sequence 41, Appl	C 350	15.6	55.7	601	4	US-09-949-016-157542	Sequence 157542, A
C 278	16	57.1	22976	4	US-09-269-939A-19	Sequence 19, Appl	C 351	15.6	55.7	601	4	US-09-949-016-157543	Sequence 157543, A
C 279	16	57.1	23187	4	US-09-499-522-1	Sequence 1, Appl	C 352	15.6	55.7	601	4	US-09-949-016-160157	Sequence 160157, A
C 280	16	57.1	26159	4	US-09-949-016-13040	Sequence 13040, A	C 353	15.6	55.7	601	4	US-09-949-016-160158	Sequence 160158, A
C 281	16	57.1	32278	4	US-09-949-016-14575	Sequence 14575, A	C 354	15.6	55.7	601	4	US-09-949-016-161271	Sequence 161271, A
C 282	16	57.1	32926	4	US-09-949-016-12959	Sequence 12959, A	C 355	15.6	55.7	601	4	US-09-949-016-161272	Sequence 161272, A
C 283	16	57.1	91279	4	US-09-949-016-15446	Sequence 15446, A	C 356	15.6	55.7	601	4	US-09-949-016-188401	Sequence 188401, A
C 284	16	57.1	92227	4	US-09-949-016-11929	Sequence 11929, A	C 357	15.6	55.7	601	4	US-09-949-016-188402	Sequence 188402, A
C 285	16	57.1	92232	4	US-09-949-016-15421	Sequence 15421, A	C 358	15.6	55.7	601	4	US-09-949-016-198904	Sequence 198904, A
C 286	16	57.1	95122	4	US-09-949-016-17235	Sequence 17235, A	C 359	15.6	55.7	601	4	US-09-949-016-198905	Sequence 198905, A
C 287	16	57.1	112132	3	US-09-741-150-3	Sequence 3, Appl	C 360	15.6	55.7	816	4	US-09-248-796A-7077	Sequence 200143, A
C 288	16	57.1	112132	4	US-10-160-187-3	Sequence 3, Appl	C 361	15.6	55.7	938	4	US-09-843-472-2	Sequence 7077, Ap
C 289	16	57.1	119801	4	US-09-949-016-13453	Sequence 13453, A	C 362	15.6	55.7	1150	4	US-09-620-312D-630	Sequence 2, Appl
C 290	16	57.1	137753	4	US-09-949-016-17404	Sequence 17404, A	C 363	15.6	55.7	1263	4	US-09-724-797-37	Sequence 37, Appl
C 291	16	57.1	161900	4	US-09-949-016-12685	Sequence 12685, A	C 364	15.6	55.7	1503	3	US-08-307-499-41	Sequence 41, Appl
C 292	16	57.1	161914	4	US-09-949-016-12906	Sequence 12906, A	C 365	15.6	55.7	1503	3	US-09-299-268-41	Sequence 41, Appl
C 293	16	57.1	162841	4	US-09-949-016-13733	Sequence 13733, A	C 366	15.6	55.7	1525	4	US-09-799-451-618	Sequence 618, App
C 294	16	57.1	169334	4	US-09-949-016-15999	Sequence 15999, A	C 367	15.6	55.7	1596	3	US-09-484-970B-148	Sequence 148, App
C 295	16	57.1	183112	4	US-09-949-016-15494	Sequence 15494, A	C 368	15.6	55.7	1910	3	US-09-221-017B-234	Sequence 234, App
C 296	16	57.1	183770	4	US-09-949-016-15494	Sequence 15494, A	C 369	15.6	55.7	1920	4	US-09-902-540-6398	Sequence 6398, App
C 297	16	57.1	193555	4	US-09-949-016-15553	Sequence 15553, A	C 370	15.6	55.7	1921	4	US-09-902-540-428	Sequence 428, App
C 298	16	57.1	193555	4	US-09-949-016-15553	Sequence 15553, A	C 371	15.6	55.7	2019	4	US-09-540-236-739	Sequence 739, App
C 299	16	57.1	193555	4	US-09-949-016-15555	Sequence 15555, A	C 372	15.6	55.7	2077	4	US-09-620-312D-985	Sequence 985, App
C 300	16	57.1	211049	4	US-09-949-016-15770	Sequence 15770, A	C 373	15.6	55.7	2257	4	US-09-808-701A-2	Sequence 2, Appl
C 301	16	57.1	422592	4	US-09-949-016-14182	Sequence 14182, A	C 374	15.6	55.7	3366	1	US-08-469-802B-1	Sequence 1, Appl
C 302	16	57.1	4403765	3	US-09-103-840A-1	Sequence 2, Appl	C 375	15.6	55.7	3366	2	US-08-267-803B-1	Sequence 1, Appl
C 303	16	57.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl	C 376	15.6	55.7	3366	2	US-08-469-802B-1	Sequence 1, Appl
C 304	15.8	56.4	393	4	US-09-513-999C-2598	Sequence 2598, Ap	C 377	15.6	55.7	3602	3	US-09-402-929-1	Sequence 1, Appl
C 305	15.8	56.4	453	4	US-09-621-976-1609	Sequence 1609, Ap	C 378	15.6	55.7	3699	4	US-09-248-796A-460	Sequence 460, App
C 306	15.8	56.4	601	4	US-09-949-016-52792	Sequence 52792, A	C 379	15.6	55.7	4880	3	US-09-402-929-5	Sequence 5, Appl
C 307	15.8	56.4	601	4	US-09-949-016-15917	Sequence 15917, A	C 380	15.6	55.7	5211	1	US-08-447-411-1	Sequence 1, Appl
C 308	15.8	56.4	601	4	US-09-949-016-163712	Sequence 163712, A	C 381	15.6	55.7	6775	3	US-09-402-929-4	Sequence 4, Appl
C 309	15.8	56.4	601	4	US-09-949-016-169681	Sequence 169681, A	C 382	15.6	55.7	8040	1	US-08-596-291-1	Sequence 1, Appl
C 310	15.8	56.4	2310	4	US-09-543-681A-3003	Sequence 3003, Ap	C 383	15.6	55.7	8040	3	US-09-100-804-1	Sequence 1, Appl
C 311	15.8	56.4	2686	3	US-09-228-986-3	Sequence 3, Appl	C 384	15.6	55.7	8043	5	PCF-US94-09943-1	Sequence 1, Appl
C 312	15.8	56.4	2686	4	US-10-101-464A-3	Sequence 3, Appl	C 385	15.6	55.7	8119	3	US-09-290-640-45	Sequence 45, Appl
C 313	15.8	56.4	13261	4	US-09-949-016-15645	Sequence 15645, A	C 386	15.6	55.7	8119	3	US-09-665-615B-45	Sequence 45, Appl
C 314	15.8	56.4	14566	4	US-09-949-016-16765	Sequence 16765, A	C 387	15.6	55.7	8287	4	US-09-023-655-1441	Sequence 1441, A
C 315	15.8	56.4	19383	4	US-09-949-016-16031	Sequence 16031, A	C 388	15.6	55.7	13198	4	US-09-949-016-16425	Sequence 16425, A
C 316	15.8	56.4	21048	4	US-09-949-016-16091	Sequence 16091, A	C 389	15.6	55.7	14176	1	US-08-307-499-1	Sequence 1, Appl
C 317	15.8	56.4	27360	4	US-09-949-016-17502	Sequence 17502, A	C 390	15.6	55.7	14176	3	US-08-307-499-14	Sequence 14, Appl
C 318	15.8	56.4	35355	4	US-09-949-016-14197	Sequence 14197, A	C 391	15.6	55.7	14176	3	US-09-299-268-1	Sequence 1, Appl
C 319	15.8	56.4	42574	4	US-09-949-016-17525	Sequence 17525, A	C 392	15.6	55.7	15116	4	US-09-299-268-14	Sequence 14, Appl
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c 460 15.6 55.7 161652 4 US-09-497-855A-40 Sequence 40, Appli
c 461 15.6 55.7 176006 4 US-09-949-016-16804 Sequence 16804, A
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ALIGNMENTS

RESULT 1
US-08-869-423-1/c
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kochel, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cnd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Kalish, Daniel
REGISTRATION NUMBER: 33,599
REFERENCE/DOCKET NUMBER: NC 77,654
TELEPHONE: (301) 295-5642
TELEFAX: (301) 295-1022
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: New Guinea C
POSITION IN GENOME:
CHROMOSOME/SEGMENT: PreM and Envelope
MAP POSITION: 330-2446
UNITS: bp
PUBLICATION INFORMATION:
AUTHORS: Gruenberg, A
AUTHORS: Woo, W S
AUTHORS: Biedrzycka, A
AUTHORS: Wright, P J
TITLE: Partial nucleotide sequence and deduced amino
TITLE: acid sequence of the structural proteins of dengue
TITLE: virus type 2, New Guinea C and PUO-218 strains
JOURNAL: J. Gen. Virol.
VOLUME: 69
PAGES: 1391-1398
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Irie, K
AUTHORS: Mohan, P M
AUTHORS: Sasaguri, Y
AUTHORS: Putnak, R
AUTHORS: Padmanabhan, R
TITLE: Sequence Analysis of Cloned dengue virus type
TITLE: 2 genome (New Guinea-C strain)
JOURNAL: Gene
VOLUME: 75
ISSUE: 2
PAGES: 197-211
DATE: 1989
PUBLICATION INFORMATION:
AUTHORS: Yaegashi, T
AUTHORS: Vakharia, V N
AUTHORS: Page, K
AUTHORS: Sasaguri, Y
AUTHORS: Feignun, R
AUTHORS: Padmanabhan, R
JOURNAL: Gene
VOLUME: 46
ISSUE: 2-3
PAGES: 257-267
DATE: 1986
US-08-937-195-1
Query Match 89.3%; Score 25; DB 3; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.07;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
Db 228 CCCATCTCTTCAGTATCCCTGCTGTGG 201
RESULT 2

US-08-937-195-1/c
Sequence 1, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVI, JOHN M.
APPLICANT: KAKANO, BILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
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OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= ([1])
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LOCATION: 1929

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, LOCATION: 2326
, OTHER INFORMATION: /note= "Start of coding strand
, OTHER INFORMATION: sequence for NS1"
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, PUBLICATION INFORMATION:
, AUTHORS: Hahn, Y.S.
, JOURNAL: Virology
, VOLUME: 162
, PAGES: 167-180
, DATE: 1988
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, US-08-937-195-1
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, Query Match 77.9%; Score 21.8; DB 3; Length 3381;
, Best Local Similarity 82.1%; Pred. No. 2.3;
, Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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, Qy 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
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, Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181
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, RESULT 3
, US-08-937-195-2/c
, Sequence 2, Application US/08937195
, Patent No. 6136561
, GENERAL INFORMATION:
, APPLICANT: IVY, JOHN M.
, APPLICANT: KAKANO, EILEEN
, APPLICANT: CLEMENTS, DAVID
, TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
, NUMBER OF SEQUENCES: 18
, CORRESPONDENCE ADDRESS:
, ADDRESSEE: MORRISON & FOERSTER
, STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
, CITY: WASHINGTON
, STATE: DC
, COUNTRY: USA
, ZIP: 20006-1812
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/937,195
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, FILING DATE:
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APLICATION NUMBER: US 08/488,807
, FILING DATE: 07-JUN-1995
, ATTORNEY/AGENT INFORMATION:
, NAME: MURASHIGE, KATE H.
, REGISTRATION NUMBER: 29,959
, REFERENCE/DOCKET NUMBER: 4733-0003.20
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (202) 887-1500
, TELEFAX: (202) 887-0763
, TELEX: 90-4030
, INFORMATION FOR SEQ ID NO: 2:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 3381 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
, ORIGINAL SOURCE:
, ORGANISM: Dengue virus
, STRAIN: Serotype 2(DEN-2)
, IMMEDIATE SOURCE:
, CLONE: Den-2 PR159/S1
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, LOCATION: 1216..1218
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, OTHER INFORMATION: /citation= ([1])
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; LOCATION: 841
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; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
US-08-937-195-2
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181

RESULT 4
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; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
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; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ({1})
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; NAME/KEY: misc_feature
; LOCATION: 1218
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; OTHER INFORMATION: sequence for Capsid."
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
US-08-915-152-1
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181
```

RESULT 5

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US-08-915-152-2/c
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2(DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
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; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-2
;
; Query Match 77.9%; Score 21.8; DB 3; Length 3381;
; Best Local Similarity 82.1%; Pred. No. 2.3;
; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Oy 1 CCATCTCTCANNATCCCTGCTGTGG 28
; ||||| || ||||| |||||
; Db 208 CCATCTTTTAAATATCCCTGCTGTGG 181
;
; RESULT 6
; US-09-376-463-2/c
; Sequence 2, Application US/09376463
; Patent No. 6749857
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.20
; CURRENT APPLICATION NUMBER: US/09/376,463
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
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; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-09-376-463-2

Query Match 77.9%; Score 21.8; DB 4; Length 3381;
Best Local Similarity 82.1%; Pred.No.2,3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTCNTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTATATATCCCTGCTGTGG 181

RESULT 7
PCT-US96-07627-1/c
; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"

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[illegible]

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; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; PCT-US96-07627-2
;
; Query Match 77.9%; Score 21.8; DB 5; Length 3381;
; Best Local Similarity 82.1%; Pred. No. 2.3;
; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
; Db 208 CCCATCTTTTAATATCCCTGCTGTGG 181
;
; RESULT 9
; US-08-325-426B-1/c
; Sequence 1, Application US/08325426B
; Patent No. 6017535
```

```
; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
; US-08-325-426B-1
;
; Query Match 72.1%; Score 20.2; DB 3; Length 10718;
; Best Local Similarity 78.6%; Pred. No. 17;
; Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
; Db 288 CCCATCTAGCCAAATTCCTGCTGTGG 261
;
; RESULT 10
; US-07-807-043B-8
; Sequence 8, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,043B
```



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;
; FILING DATE: 19911212
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; US-07-807-043B-8

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGACGAATCCCTGCTGT 1921

RESULT 11
US-08-190-411A-1
; Sequence 1, Application US/08190411A
; Patent No. 5541104
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,411A
; FILING DATE: 01-FEBRUARY-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5541104man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; US-08-190-411A-1

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGACGAATCCCTGCTGT 1921

RESULT 12
US-08-299-849B-8
; Sequence 8, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; APPLICATION NUMBER: 9-JULY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 5612201man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5355
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5674 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: genomic DNA
;; FEATURE:
;; NAME/KEY: MAGE-1 gene
US-08-299-849B-8

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 13
US-08-560-024-1
;; Sequence 1, Application US/08560024
;; Patent No. 5843448
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Yao-Tsung; Stockert, Elisabeth;
;; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
;; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
;; APPLICANT: Old, Lloyd J.
;; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
;; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
;; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Felfe & Lynch
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; ZIP: 10022
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/560,024
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/190,411
;; FILING DATE: 01-FEBRUARY-1994
;; APPLICATION NUMBER: 037,230
;; FILING DATE: 26-MARCH-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/04354
;; FILING DATE: 22-MAY-1992
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 07/807,043
;; FILING DATE: 12-DECEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; APPLICATION NUMBER: 9-JULY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 5843448man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5354
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5674 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: genomic DNA
;; FEATURE:
;; NAME/KEY: MAGE-1 gene
US-08-560-024-1

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 14
US-08-142-368A-8
;; Sequence 8, Application US/08142368A
;; Patent No. 5925729
;; GENERAL INFORMATION:
;; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
;; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
;; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Felfe & Lynch
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; ZIP: 10022
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/142,368A
;; FILING DATE: 02-MAY-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/04354
;; FILING DATE: 22-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/807,043
;; FILING DATE: 12-DECEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5925729man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.4-US
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-142-368A-8

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 15
US-08-967-727-8
; Sequence 8, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-967-727-8

Query Match 67.1%; Score 18.8; DB 3; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 16
US-08-037-230D-8
; Sequence 8, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6235525man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353

, PRIOR APPLICATION DATA: ,
 , APPLICATION NUMBER: 07/705,702 ,
 , FILING DATE: 23-MAY-1991 ,
 , ATTORNEY/AGENT INFORMATION: ,
 , NAME: Hanson, No. 649021man D. ,
 , REGISTRATION NUMBER: 30,946 ,
 , REFERENCE/DOCKET NUMBER: LUD 5353 ,
 , TELECOMMUNICATION INFORMATION: ,
 , TELEPHONE: (212) 688-9200 ,
 , TELEFAX: (212) 838-3884 ,
 , INFORMATION FOR SEQ ID NO: 8: ,

US-09-579-197-8

Query Match 67.1%; Score 18.8; DB 4; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGAAATCCCTGCTGT 1921

RESULT 19
US-09-404-026-8
; Sequence 8, Application US/09404026
; Patent No. 6565857
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: Boon-Falieu, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/404,026
; FILING DATE: 23-SEPT-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6565857man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-09-404-026-8

Query Match 67.1%; Score 18.8; DB 4; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGAAATCCCTGCTGT 1921

RESULT 20
US-09-312-464-8
; Sequence 8, Application US/09312464
; Patent No. 6599699
; GENERAL INFORMATION:
; APPLICANT: Van den Eynde, Benoit; van der Bruggen, Pierre;
; APPLICANT: Boon-Falieu, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-2 AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: <Unknown>
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,464
; FILING DATE: 17-May-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,727
; FILING DATE: 27-NOVEMBER-1997
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6599699man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.5-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)318-3168
; TELEFAX: (212)752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-312-464-8

Query Match 67.1%; Score 18.8; DB 4; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGAAATCCCTGCTGT 1921

Db 1897 CTCATCTTGTGAGAAATCCCTGCTGT 1921

RESULT 21

US-09-949-016-12445

; Sequence 12445, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12445

; LENGTH: 5699

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-12445

Query Match 67.1%; Score 18.8; DB 4; Length 5699;

Best Local Similarity 80.0%; Pred. No. 64;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTTCNATCCCTGCTGT 25

Db 231 CTCATCTTGTGAGAAATCCCTGCTGT 255

RESULT 22

US-09-949-016-14430

; Sequence 14430, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14430

; LENGTH: 5699

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14430

Query Match 67.1%; Score 18.8; DB 4; Length 5699;

Best Local Similarity 80.0%; Pred. No. 64;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTTCNATCCCTGCTGT 25

Db 231 CTCATCTTGTGAGAAATCCCTGCTGT 255

RESULT 23

US-08-472-809B-8

; Sequence 8, Application US/08472809B

; Patent No. 5925564

; GENERAL INFORMATION:

; APPLICANT: Schwartz, Robert J.

; APPLICANT: DeMayo, Franco J.

; APPLICANT: O'Malley, Bert W.

; TITLE OF INVENTION: Expression Vector Systems and

; TITLE OF INVENTION: Method of Use

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,809B

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/209,846

; FILING DATE: March 9, 1994

; APPLICATION NUMBER: 07/789,919

; FILING DATE: No. 5925564ember 6, 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 214/212

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5707 bases

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-08-472-809B-8

Query Match 67.1%; Score 18.8; DB 2; Length 5707;

Best Local Similarity 80.0%; Pred. No. 64;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATCTCATTCCCTGCTGTGG 28

Db 3092 ATCTCATCATCTCCCTGCTGTGG 3116

RESULT 24

US-08-472-809B-7

; Sequence 7, Application US/08472809B

; Patent No. 5925564

; GENERAL INFORMATION:

; APPLICANT: Schwartz, Robert J.

; APPLICANT: DeMayo, Franco J.

; APPLICANT: O'Malley, Bert W.

; TITLE OF INVENTION: Expression Vector Systems and

; TITLE OF INVENTION: Method of Use

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,809B

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/209,846

; FILING DATE: March 9, 1994

; APPLICATION NUMBER: 07/789,919

; FILING DATE: No. 5925564ember 6, 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 214/212

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5707 bases

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-08-472-809B-8

Query Match	66.4%	Score 18.6;	DB 4;	Length 601;
Best Local Similarity	75.0%	Pred. No. 46;		
Matches 21;	Conservative	0;	Mismatches	7;
			Indels	0;
			Gaps	0;

Query Match 66.4%; Score 18.6; DB 4; Length 767677;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTTGG 28
DB 366317 CCCACCTCTCCCATCCCTGCTGTTGG 366290

RESULT 28
US-09-949-016-108599
; Sequence 108599, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108599
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108599

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTT 26
DB 440 CCCCTCTCTCAGTCTCTCTGCTGTT 465

RESULT 29
US-09-949-016-2987/c
; Sequence 2987, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2987
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2987

Query Match 65.0%; Score 18.2; DB 4; Length 2290;
Best Local Similarity 76.9%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTT 26

DB 1464 CCCCTCTCTCAGTCTCTCTGCTGTT 1439

RESULT 30
US-08-437-607A-3/c
; Sequence 3, Application US/08437607A
; Patent No. 555579
; GENERAL INFORMATION:
; APPLICANT: Leonard, James N. Montminy, Marc R.
; TITLE OF INVENTION: ISLET-SPECIFIC HOMEOPROTEIN AND TRANSCRIPTIONAL
; REGULATOR OF INSULIN GENE EXPRESSION
; NUMBER OF INVENTIONS: 49
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,607A
; FILING DATE: MAY 9, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1110-1-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2917 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Human HoxB13 gene
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 582..1184
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1185..2132
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2133..2384
US-08-437-607A-3

Query Match 65.0%; Score 18.2; DB 2; Length 2917;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTT 26
DB 2859 CCCCTCTCTCAGTCTCTCTGCTGTT 2834

RESULT 31
US-09-439-313-333/c
; Sequence 333, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun


```
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-333

Query Match          65.0%; Score 18.2; DB 3; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches    20; Conservative   0; Mismatches    6; Indels    0; Gaps    0;

QY      1 CCCATCTCNTCANNATCCCGTGTGTT 26
           ||| |||| ||| ||| |||||||
Db     1455 CCCTTCCTCACTCTTCCTGCTGTT 1430

RESULT 34
US-09-636-215-333/C
; Sequence 333, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Ajjun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-333

Query Match          65.0%; Score 18.2; DB 4; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches    20; Conservative   0; Mismatches    6; Indels    0; Gaps    0;

QY      1 CCCATCTCNTCANNATCCCGTGTGTT 26
           ||| |||| ||| ||| |||||||
Db     1455 CCCTTCCTCACTCTTCCTGCTGTT 1430

RESULT 35
US-09-685-166A-333/c
; Sequence 333, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

RESULT 37
US-09-679-426-333/c
; Sequence 333, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

RESULT 38
 US-09-759-143-333/c
 ; Sequence 333, Application US/09759143
 ; Patent No. 6800746
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 333
 ; LENGTH: 3030
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-759-143-333

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RESULT 40
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 ; Sequence 14729, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14729
 ; LENGTH: 7242

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Title: US-10-085-944-1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 18, Appli					
Sequence 14, Appli					
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Sequence 30, Appli					

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85	17.6	62.9	1514	9	US-09-738-546-1	Sequence 1, Appl	c 158	17.2	61.4	23587	10	US-09-764-891-9788	Sequence 9788, App
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134	17.2	61.4	1519	17	US-10-341-434-179	Sequence 179, App	c 207	17.2	60.7	121	17	US-10-261-185-1852	Sequence 1852, App
135	17.2	61.4	1519	17	US-10-693-999-22	Sequence 22, Appl	c 208	17.2	60.7	121	17	US-10-261-185-1853	Sequence 1853, App
136	17.2	61.4	1581	19	US-10-437-963-62172	Sequence 62172, A	c 209	17.2	60.7	121	17	US-10-261-185-1856	Sequence 1856, App
137	17.2	61.4	1638	17	US-10-369-493-45046	Sequence 45046, A	c 210	17.2	60.7	121	17	US-10-261-185-1857	Sequence 1857, App
138	17.2	61.4	1927	14	US-10-453-668-379	Sequence 379, App	c 211	17.2	60.7	121	17	US-10-261-185-1860	Sequence 1860, App
139	17.2	61.4	1927	14	US-10-453-668-381	Sequence 381, App	c 212	17.2	60.7	121	17	US-10-261-185-1861	Sequence 1861, App
140	17.2	61.4	2154	19	US-10-437-963-12481	Sequence 12481, A	c 213	17.2	60.7	121	17	US-10-261-185-1864	Sequence 1864, App
141	17.2	61.4	3294	19	US-10-437-963-62175	Sequence 62175, A	c 214	17.2	60.7	121	17	US-10-261-185-1865	Sequence 1865, App
142	17.2	61.4	4090	19	US-10-437-963-51235	Sequence 51235, A	c 215	17.2	60.7	121	17	US-10-261-185-1868	Sequence 1868, App
143	17.2	61.4	4119	10	US-09-764-891-6600	Sequence 6600, App	c 216	17.2	60.7	121	17	US-10-261-185-1869	Sequence 1869, App
144	17.2	61.4	4119	14	US-10-091-572-464	Sequence 464, App	c 217	17.2	60.7	121	17	US-10-261-185-1872	Sequence 1872, App
145	17.2	61.4	4124	10	US-09-764-891-6599	Sequence 6599, App	c 218	17.2	60.7	121	17	US-10-261-185-1873	Sequence 1873, App
146	17.2	61.4	4124	14	US-10-091-572-463	Sequence 463, App	c 219	17.2	60.7	121	17	US-10-261-185-1876	Sequence 1876, App
147	17.2	61.4	5358	19	US-10-437-963-24917	Sequence 24917, A	c 220	17.2	60.7	121	17	US-10-261-185-1877	Sequence 1877, App
148	17.2	61.4	5781	15	US-10-399-058-1	Sequence 1, Appl	c 221	17.2	60.7	121	19	US-10-681-074-1844	Sequence 1844, App
149	17.2	61.4	5781	15	US-10-399-058-3	Sequence 3, Appl	c 222	17.2	60.7	121	19	US-10-681-074-1845	Sequence 1845, App
150	17.2	61.4	6204	9	US-09-880-107-3036	Sequence 3036, App	c 223	17.2	60.7	121	19	US-10-681-074-1848	Sequence 1848, App
151	17.2	61.4	6204	17	US-10-372-683-3	Sequence 3, Appl	c 224	17.2	60.7	121	19	US-10-681-074-1849	Sequence 1849, App
152	17.2	61.4	6297	21	US-10-956-157-820	Sequence 820, App	c 225	17.2	60.7	121	19	US-10-681-074-1852	Sequence 1852, App
153	17.2	61.4	6482	18	US-10-363-616-212	Sequence 212, App	c 226	17.2	60.7	121	19	US-10-681-074-1853	Sequence 1853, App

227	17	60.7	121	19	US-10-681-074-1855	Sequence 1856, Ap	c 300	17	60.7	807	17	US-10-369-493-45415	Sequence 45415, A
c 228	17	60.7	121	19	US-10-681-074-1857	Sequence 1857, Ap	c 301	17	60.7	860	17	US-10-767-701-12334	Sequence 12334, A
c 229	17	60.7	121	19	US-10-681-074-1860	Sequence 1860, Ap	c 302	17	60.7	868	13	US-10-027-632-138164	Sequence 138164, A
c 230	17	60.7	121	19	US-10-681-074-1861	Sequence 1861, Ap	c 303	17	60.7	868	13	US-10-027-632-138165	Sequence 138165, A
c 231	17	60.7	121	19	US-10-681-074-1864	Sequence 1864, Ap	c 304	17	60.7	868	17	US-10-027-632-138164	Sequence 138164, A
c 232	17	60.7	121	19	US-10-681-074-1865	Sequence 1865, Ap	c 305	17	60.7	868	17	US-10-027-632-138165	Sequence 138165, A
c 233	17	60.7	121	19	US-10-681-074-1868	Sequence 1868, Ap	c 306	17	60.7	1125	19	US-10-437-963-10123	Sequence 10123, A
c 234	17	60.7	121	19	US-10-681-074-1869	Sequence 1869, Ap	c 307	17	60.7	1422	15	US-10-081-872-163	Sequence 163, App
c 235	17	60.7	121	19	US-10-681-074-1872	Sequence 1872, Ap	c 308	17	60.7	1422	19	US-10-385-305-163	Sequence 163, App
c 236	17	60.7	121	19	US-10-681-074-1873	Sequence 1873, Ap	c 309	17	60.7	1725	19	US-10-437-963-90255	Sequence 90255, A
c 237	17	60.7	121	19	US-10-681-074-1876	Sequence 1876, Ap	c 310	17	60.7	1893	19	US-10-437-963-20390	Sequence 20390, A
c 238	17	60.7	121	19	US-10-681-074-1877	Sequence 1877, Ap	c 311	17	60.7	2000	17	US-10-260-238-2159	Sequence 2159, A
c 239	17	60.7	201	20	US-10-719-993-8083	Sequence 8083, Ap	c 312	17	60.7	2163	19	US-10-437-963-39821	Sequence 39821, A
c 240	17	60.7	201	20	US-10-719-993-8679	Sequence 8679, Ap	c 313	17	60.7	2218	19	US-10-437-963-41458	Sequence 41458, A
c 241	17	60.7	201	21	US-10-741-600-6107	Sequence 6107, Ap	c 314	17	60.7	4371	21	US-10-813-507-12	Sequence 12, Appl
c 242	17	60.7	201	21	US-10-741-600-6108	Sequence 6108, Ap	c 315	17	60.7	4629	9	US-09-150-811-7	GENERAL INFO
c 243	17	60.7	201	21	US-10-741-600-6113	Sequence 6113, Ap	c 316	17	60.7	4999	9	US-09-740-211-14	Sequence 14, Appl
c 244	17	60.7	201	21	US-10-741-600-6184	Sequence 6184, Ap	c 317	17	60.7	4999	14	US-10-007-968-14	Sequence 14, Appl
c 245	17	60.7	201	21	US-10-741-600-6214	Sequence 6214, Ap	c 318	17	60.7	4999	14	US-10-293-400-14	Sequence 14, Appl
c 246	17	60.7	201	21	US-10-741-600-6234	Sequence 6234, Ap	c 319	17	60.7	6996	17	US-10-239-498A-1	Sequence 1, Appl
c 247	17	60.7	201	21	US-10-741-600-6236	Sequence 6236, Ap	c 320	17	60.7	6996	21	US-10-813-507-7	Sequence 7, Appl
c 248	17	60.7	201	21	US-10-741-600-6239	Sequence 6239, Ap	c 321	17	60.7	7931	18	US-10-411-037-29	Sequence 29, Appl
c 249	17	60.7	201	21	US-10-741-600-6240	Sequence 6240, Ap	c 322	17	60.7	7931	18	US-10-411-026-29	Sequence 29, Appl
c 250	17	60.7	201	21	US-10-741-600-6241	Sequence 6241, Ap	c 323	17	60.7	7931	18	US-10-410-962-29	Sequence 29, Appl
c 251	17	60.7	201	21	US-10-741-600-6242	Sequence 6242, Ap	c 324	17	60.7	7931	18	US-10-411-049-29	Sequence 29, Appl
c 252	17	60.7	201	21	US-10-741-600-6247	Sequence 6247, Ap	c 325	17	60.7	7931	18	US-10-410-930-29	Sequence 29, Appl
c 253	17	60.7	201	21	US-10-741-600-6253	Sequence 6253, Ap	c 326	17	60.7	7931	19	US-10-410-997-29	Sequence 29, Appl
c 254	17	60.7	201	21	US-10-741-600-6254	Sequence 6254, Ap	c 327	17	60.7	7931	19	US-10-411-012-29	Sequence 29, Appl
c 255	17	60.7	201	21	US-10-741-600-6256	Sequence 6256, Ap	c 328	17	60.7	7931	19	US-10-287-994-29	Sequence 29, Appl
c 256	17	60.7	201	21	US-10-741-600-6508	Sequence 6508, Ap	c 329	17	60.7	7931	19	US-10-410-913-29	Sequence 29, Appl
c 257	17	60.7	201	21	US-10-741-600-6509	Sequence 6509, Ap	c 330	17	60.7	7931	21	US-10-410-980-29	Sequence 29, Appl
c 258	17	60.7	201	21	US-10-741-600-6514	Sequence 6514, Ap	c 331	17	60.7	7931	21	US-10-410-897-29	Sequence 29, Appl
c 259	17	60.7	201	21	US-10-741-600-6585	Sequence 6585, Ap	c 332	17	60.7	7931	21	US-10-410-921-29	Sequence 29, Appl
c 260	17	60.7	201	21	US-10-741-600-6641	Sequence 6641, Ap	c 333	17	60.7	7931	21	US-10-492-261-29	Sequence 29, Appl
c 261	17	60.7	201	21	US-10-741-600-6635	Sequence 6635, Ap	c 334	17	60.7	7944	18	US-10-681-970A-3	Sequence 1, Appl
c 262	17	60.7	201	21	US-10-741-600-6637	Sequence 6637, Ap	c 335	17	60.7	8720	17	US-10-239-498A-14	Sequence 14, Appl
c 263	17	60.7	201	21	US-10-741-600-6640	Sequence 6640, Ap	c 336	17	60.7	8967	20	US-10-472-516-1	Sequence 1, Appl
c 264	17	60.7	201	21	US-10-741-600-6641	Sequence 6641, Ap	c 337	17	60.7	8967	20	US-10-968-286-1	Sequence 1, Appl
c 265	17	60.7	201	21	US-10-741-600-6642	Sequence 6642, Ap	c 338	17	60.7	9009	9	US-09-957-641-1	Sequence 1, Appl
c 266	17	60.7	201	21	US-10-741-600-6643	Sequence 6643, Ap	c 339	17	60.7	9009	14	US-10-187-319-1	Sequence 1, Appl
c 267	17	60.7	201	21	US-10-741-600-6648	Sequence 6648, Ap	c 340	17	60.7	9009	16	US-10-131-510A-1	Sequence 1, Appl
c 268	17	60.7	201	21	US-10-741-600-6654	Sequence 6654, Ap	c 341	17	60.7	9009	17	US-10-445-235-1	Sequence 1, Appl
c 269	17	60.7	201	21	US-10-741-600-6655	Sequence 6655, Ap	c 342	17	60.7	9009	20	US-10-491-464-1	Sequence 1, Appl
c 270	17	60.7	201	21	US-10-741-600-6657	Sequence 6657, Ap	c 343	17	60.7	9009	21	US-10-938-414-1	Sequence 1, Appl
c 271	17	60.7	201	21	US-10-741-600-27914	Sequence 27914, A	c 344	17	60.7	9009	22	US-10-813-507-5	Sequence 5, Appl
c 272	17	60.7	201	21	US-10-741-600-27915	Sequence 27915, A	c 345	17	60.7	9009	22	US-10-973-941-1	Sequence 1, Appl
c 273	17	60.7	201	21	US-10-741-600-28012	Sequence 28012, A	c 346	17	60.7	9029	14	US-10-181-875-10	Sequence 10, Appl
c 274	17	60.7	201	21	US-10-741-600-28052	Sequence 28052, A	c 347	17	60.7	9029	15	US-10-871-775-32	Sequence 32, Appl
c 275	17	60.7	201	21	US-10-741-600-28074	Sequence 28074, A	c 348	17	60.7	9030	21	US-10-133-907-1	Sequence 1, Appl
c 276	17	60.7	201	21	US-10-741-600-28077	Sequence 28077, A	c 349	17	60.7	9164	17	US-10-804-763-39	Sequence 39, Appl
c 277	17	60.7	201	21	US-10-741-600-28079	Sequence 28079, A	c 350	17	60.7	9164	17	US-10-411-711-2	Sequence 2, Appl
c 278	17	60.7	201	21	US-10-741-600-28090	Sequence 28090, A	c 351	17	60.7	10698	17	US-10-239-498A-12	Sequence 12, Appl
c 279	17	60.7	263	20	US-10-425-115-149847	Sequence 149847, A	c 352	17	60.7	11846	17	US-10-239-498A-14	Sequence 14, Appl
c 280	17	60.7	306	13	US-10-016-157A-143	Sequence 143, App	c 353	17	60.7	11933	9	US-10-411-711-4	Sequence 4, Appl
c 281	17	60.7	330	19	US-10-437-963-77253	Sequence 77253, A	c 354	17	60.7	11933	13	US-09-740-211-13	Sequence 13, Appl
c 282	17	60.7	405	11	US-09-864-408A-6095	Sequence 6095, A	c 355	17	60.7	11933	14	US-10-007-968-13	Sequence 13, Appl
c 283	17	60.7	494	13	US-10-016-157A-144	Sequence 144, App	c 356	17	60.7	12022	17	US-10-293-400-13	Sequence 3, Appl
c 284	17	60.7	497	10	US-09-770-961-490	Sequence 140, App	c 357	17	60.7	12394	17	US-10-411-711-3	Sequence 10, Appl
c 285	17	60.7	504	16	US-10-029-386-8448	Sequence 8448, Ap	c 358	17	60.7	12394	17	US-10-181-875-10	Sequence 10, Appl
c 286	17	60.7	524	16	US-10-029-386-6688	Sequence 6688, Ap	c 359	17	60.7	15053	21	US-10-871-775-32	Sequence 32, Appl
c 287	17	60.7	525	13	US-10-027-632-132942	Sequence 132942, A	c 360	17	60.7	19640	13	US-10-087-192-1084	Sequence 1084, Ap
c 288	17	60.7	525	19	US-10-027-632-132942	Sequence 132942, A	c 361	17	60.7	23640	13	US-10-087-192-1249	Sequence 1249, Ap
c 289	17	60.7	555	19	US-10-437-963-37904	Sequence 37904, A	c 362	17	60.7	24261	19	US-10-331-053-7	Sequence 7, Appl
c 290	17	60.7	566	9	US-09-864-761-16832	Sequence 16832, A	c 363	17	60.7	34760	20	US-10-629-318-36	Sequence 36, Appl
c 291	17	60.7	620	13	US-10-027-632-236610	Sequence 236610, A	c 364	17	60.7	34760	20	US-10-719-993-7047	Sequence 7047, Ap
c 292	17	60.7	620	13	US-10-027-632-236611	Sequence 236611, A	c 365	17	60.7	55998	11	US-09-997-722-241	Sequence 241, App
c 293	17	60.7	620	13	US-10-027-632-236612	Sequence 236612, A	c 366	17	60.7	111084	20	US-10-723-860-1627	Sequence 1627, Ap
c 294	17	60.7	620	17	US-10-027-632-236610	Sequence 236610, A	c 367	17	60.7	140152	20	US-10-684-422-66	Sequence 66, Appl
c 295	17	60.7	620	17	US-10-027-632-236611	Sequence 236611, A	c 368	17	60.7	154394	20	US-10-723-860-601	Sequence 601, App
c 296	17	60.7	620	17	US-10-027-632-236612	Sequence 236612, A	c 369	17	60.7	181684	13	US-10-087-192-790	Sequence 790, App
c 297	17	60.7	704	21	US-10-956-157-3910	Sequence 3910, Ap	c 370	17	60.7	193691	20	US-10-719-993-6768	Sequence 6768, Ap
c 298	17	60.7	704	21	US-10-956-157-3910	Sequence 3910, Ap	c 371	17	60.7	209484	13	US-10-087-192-418	Sequence 418, App
c 299	17	60.7	721	20	US-10-425-115-167033	Sequence 167033, A	c 372	17	60.7	209484	13	US-10-331-053-4	Sequence 4, Appl
	17	60.7	721	20	US-10-425-115-167033	Sequence 167033, A		17	60.7	318760	20	US-10-719-993-6765	Sequence 6765, Ap

c 373	17	60.7	405660	19	US-10-322-696-82	Sequence 82, Appl	446	16.6	59.3	600	22	US-10-972-079-36217	Sequence 36217, A
c 374	17	60.7	606398	20	US-10-719-993-6782	Sequence 6782, Ap	447	16.6	59.3	600	22	US-10-972-079-36218	Sequence 36218, A
c 375	17	60.7	1601042	13	US-10-027-632-59064	Sequence 59064, A	448	16.6	59.3	600	22	US-10-972-079-36219	Sequence 36219, A
c 376	17	60.7	1601042	17	US-10-027-632-59084	Sequence 59084, A	449	16.6	59.3	601	22	US-10-893-315-587	Sequence 587, App
c 377	16.8	60.0	201	21	US-10-741-600-64792	Sequence 64792, A	450	16.6	59.3	601	22	US-10-893-315-1814	Sequence 1814, Ap
c 378	16.8	60.0	281	19	US-10-437-963-85226	Sequence 85226, A	c 451	16.6	59.3	619	9	US-09-770-149-796	Sequence 796, App
c 379	16.8	60.0	297	9	US-09-294-093B-2659	Sequence 2659, Ap	c 452	16.6	59.3	677	18	US-09-974-300-2380	Sequence 2380, Ap
c 380	16.8	60.0	344	20	US-10-425-115-5918	Sequence 5918, Ap	c 453	16.6	59.3	687	9	US-10-424-599-44145	Sequence 44145, A
c 381	16.8	60.0	437	10	US-09-764-891-8578	Sequence 8578, Ap	c 454	16.6	59.3	696	13	US-10-027-632-23555	Sequence 23555, A
c 382	16.8	60.0	437	10	US-09-764-891-8580	Sequence 8580, Ap	c 455	16.6	59.3	696	13	US-10-027-632-23556	Sequence 23556, A
c 383	16.8	60.0	448	11	US-09-987-899-6759	Sequence 6759, Ap	c 456	16.6	59.3	696	17	US-10-027-632-23556	Sequence 23556, A
c 384	16.8	60.0	451	13	US-10-027-632-130383	Sequence 130383, A	c 457	16.6	59.3	762	21	US-10-927-644-4	Sequence 4, Appl
c 385	16.8	60.0	451	13	US-10-027-632-130383	Sequence 130383, A	c 458	16.6	59.3	772	17	US-10-282-122A-37097	Sequence 37097, A
c 386	16.8	60.0	552	22	US-10-972-079-82300	Sequence 82300, A	c 459	16.6	59.3	772	17	US-10-282-122A-39167	Sequence 39167, A
c 387	16.8	60.0	666	13	US-10-027-632-261431	Sequence 261431, A	c 460	16.6	59.3	774	17	US-10-282-122A-40098	Sequence 40098, A
c 388	16.8	60.0	666	13	US-10-027-632-261431	Sequence 261431, A	c 461	16.6	59.3	774	17	US-10-282-122A-40098	Sequence 40098, A
c 389	16.8	60.0	1102	20	US-10-425-115-130133	Sequence 130133, A	462	16.6	59.3	916	19	US-10-767-701-8589	Sequence 8589, Ap
c 390	16.8	60.0	1233	20	US-10-425-115-130133	Sequence 130133, A	463	16.6	59.3	956	18	US-10-425-114-3385	Sequence 3385, Ap
c 391	16.8	60.0	1453	18	US-10-425-115-13203	Sequence 13203, A	c 464	16.6	59.3	1039	18	US-10-424-599-44144	Sequence 44144, A
c 392	16.8	60.0	1527	19	US-10-424-599-1735	Sequence 1735, Ap	c 465	16.6	59.3	1086	20	US-10-411-910A-339	Sequence 339, App
c 393	16.8	60.0	3284	18	US-10-424-599-1737	Sequence 1737, Ap	c 466	16.6	59.3	1116	10	US-09-875-076-23	Sequence 23, Appl
c 394	16.8	60.0	19951	20	US-10-475-502-10	Sequence 10, Appl	c 467	16.6	59.3	1116	10	US-09-875-076-23	Sequence 23, Appl
c 395	16.8	60.0	49634	11	US-09-968-007A-514	Sequence 514, App	c 468	16.6	59.3	1116	15	US-10-393-807-23	Sequence 23, Appl
c 396	16.8	60.0	49634	21	US-10-843-641A-6984	Sequence 6984, Ap	c 469	16.6	59.3	1116	16	US-10-393-807-23	Sequence 23, Appl
c 397	16.8	60.0	54016	21	US-10-741-600-17886	Sequence 17886, A	c 470	16.6	59.3	1116	17	US-10-417-820A-25	Sequence 25, Appl
c 398	16.8	60.0	123192	14	US-10-175-523-71	Sequence 71, Appl	c 471	16.6	59.3	1116	19	US-10-723-955-25	Sequence 25, Appl
c 399	16.8	60.0	358246	17	US-10-292-798-1095	Sequence 1095, Ap	c 472	16.6	59.3	1116	19	US-10-723-955-25	Sequence 25, Appl
c 400	16.8	60.0	744802	17	US-10-292-798-1369	Sequence 1369, Ap	c 473	16.6	59.3	1149	18	US-10-424-599-107235	Sequence 107235, A
c 401	16.8	60.0	9025608	15	US-10-156-761-1	Sequence 1, Appl	c 474	16.6	59.3	1172	20	US-10-425-115-445764	Sequence 445764, A
c 402	16.6	59.3	138	16	US-10-029-386-21966	Sequence 21966, A	c 475	16.6	59.3	1172	20	US-10-425-115-445764	Sequence 445764, A
c 403	16.6	59.3	197	9	US-09-796-692-7629	Sequence 7629, Ap	c 476	16.6	59.3	1205	17	US-10-027-632-31534	Sequence 31534, A
c 404	16.6	59.3	197	14	US-10-040-862-7629	Sequence 7629, Ap	c 477	16.6	59.3	1205	17	US-10-027-632-31534	Sequence 31534, A
c 405	16.6	59.3	197	17	US-10-057-475B-7629	Sequence 7629, Ap	c 478	16.6	59.3	1276	22	US-10-893-315-48	Sequence 48, Appl
c 406	16.6	59.3	197	17	US-10-154-884B-7629	Sequence 7629, Ap	c 479	16.6	59.3	1277	21	US-09-969-708-547	Sequence 547, App
c 407	16.6	59.3	197	19	US-10-764-324-7629	Sequence 7629, Ap	c 480	16.6	59.3	1277	21	US-10-843-641A-8018	Sequence 8018, Ap
c 408	16.6	59.3	201	21	US-10-741-600-6109	Sequence 6109, Ap	c 481	16.6	59.3	1277	22	US-10-893-315-19	Sequence 19, Appl
c 409	16.6	59.3	201	21	US-10-741-600-6109	Sequence 6109, Ap	c 482	16.6	59.3	1285	13	US-10-027-632-253201	Sequence 253201, A
c 410	16.6	59.3	201	21	US-10-741-600-6510	Sequence 6510, Ap	c 483	16.6	59.3	1285	17	US-10-027-632-253201	Sequence 253201, A
c 411	16.6	59.3	201	21	US-10-741-600-6510	Sequence 6510, Ap	c 484	16.6	59.3	1298	18	US-10-424-599-32001	Sequence 32001, A
c 412	16.6	59.3	201	21	US-10-741-600-6514	Sequence 6514, Ap	c 485	16.6	59.3	1318	19	US-10-437-963-44339	Sequence 44339, A
c 413	16.6	59.3	201	21	US-10-741-600-27916	Sequence 27916, A	c 486	16.6	59.3	1379	17	US-10-094-466-43	Sequence 130, Appl
c 414	16.6	59.3	271	11	US-10-741-600-28051	Sequence 28051, A	c 487	16.6	59.3	1391	9	US-09-799-777-120	Sequence 120, App
c 415	16.6	59.3	324	21	US-09-155-106-29	Sequence 29, Appl	c 488	16.6	59.3	1391	9	US-09-795-333-1	Sequence 1, Appl
c 416	16.6	59.3	324	21	US-10-808-538-29	Sequence 29, Appl	c 489	16.6	59.3	1464	17	US-10-369-493-26758	Sequence 26758, A
c 417	16.6	59.3	369	19	US-10-437-963-97495	Sequence 97495, A	c 490	16.6	59.3	1504	9	US-09-917-800A-1576	Sequence 1576, Ap
c 418	16.6	59.3	411	20	US-10-425-115-130050	Sequence 130050, A	c 491	16.6	59.3	1504	17	US-10-191-803-41	Sequence 41, Appl
c 419	16.6	59.3	413	11	US-09-864-408A-8137	Sequence 8137, Ap	c 492	16.6	59.3	1504	18	US-10-152-319A-1546	Sequence 1546, Ap
c 420	16.6	59.3	451	21	US-10-696-639-2711	Sequence 2711, Ap	c 493	16.6	59.3	1504	21	US-10-486-706-238	Sequence 238, App
c 421	16.6	59.3	453	20	US-10-425-115-13784	Sequence 13784, A	c 494	16.6	59.3	1543	20	US-10-653-047-5534	Sequence 5534, Ap
c 422	16.6	59.3	458	16	US-10-002-631C-115	Sequence 115, App	c 495	16.6	59.3	1607	18	US-10-425-114-20398	Sequence 20398, A
c 423	16.6	59.3	482	10	US-09-918-995-348	Sequence 348, App	c 496	16.6	59.3	1649	17	US-10-094-466-15	Sequence 15, Appl
c 424	16.6	59.3	474	9	US-09-864-761-1860	Sequence 1860, App	c 497	16.6	59.3	1733	20	US-10-425-115-45003	Sequence 45003, A
c 425	16.6	59.3	480	13	US-10-027-632-281125	Sequence 281125, A	c 498	16.6	59.3	1735	19	US-10-437-963-48439	Sequence 48439, A
c 426	16.6	59.3	480	17	US-10-027-632-281125	Sequence 281125, A	c 499	16.6	59.3	1760	18	US-10-424-599-72220	Sequence 72220, A
c 427	16.6	59.3	480	19	US-10-437-963-44341	Sequence 44341, A	c 500	16.6	59.3	1764	13	US-10-027-632-97663	Sequence 97663, A
c 428	16.6	59.3	503	9	US-09-864-761-16617	Sequence 16617, A							
c 429	16.6	59.3	503	9	US-09-864-761-18610	Sequence 18610, A							
c 430	16.6	59.3	503	16	US-10-029-386-9388	Sequence 9388, Ap							
c 431	16.6	59.3	506	13	US-10-027-632-281859	Sequence 281859, A							
c 432	16.6	59.3	506	17	US-10-027-632-281859	Sequence 281859, A							
c 433	16.6	59.3	516	16	US-10-029-386-8266	Sequence 8266, Ap							
c 434	16.6	59.3	533	22	US-10-972-079-91737	Sequence 91737, A							
c 435	16.6	59.3	534	13	US-10-027-632-281778	Sequence 281778, A							
c 436	16.6	59.3	534	17	US-10-027-632-281778	Sequence 281778, A							
c 437	16.6	59.3	577	18	US-10-424-599-94002	Sequence 94002, A							
c 438	16.6	59.3	585	13	US-10-027-632-185504	Sequence 185504, A							
c 439	16.6	59.3	585	17	US-10-027-632-185504	Sequence 185504, A							
c 440	16.6	59.3	597	20	US-10-425-115-139907	Sequence 139907, A							
c 441	16.6	59.3	597	22	US-10-972-079-72609	Sequence 72609, A							
c 442	16.6	59.3	600	22	US-10-972-079-22441	Sequence 22441, A							
c 443	16.6	59.3	600	22	US-10-972-079-22442	Sequence 22442, A							
c 444	16.6	59.3	600	22	US-10-972-079-36215	Sequence 36215, A							
c 445	16.6	59.3	600	22	US-10-972-079-36216	Sequence 36216, A							

ALIGNMENTS

RESULT 1
US-10-085-944-1
; Sequence 1, Application US/10085944
; Publication No. US202020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2


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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9, 13, 14
; OTHER INFORMATION: n = inosine
US-10-085-944-1

Query Match      89.3%; Score 25; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCATCTCMTCAATCCCTGCTGTTGG 28
   ||||| ||||| ||||| ||||| |||||
Db 1 CCCATCTCMTCAATCCCTGCTGTTGG 28

RESULT 2
US-10-719-547-18/c
; Sequence 18, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10616
; TYPE: DNA
; ORGANISM: Recombinant dengue virus rDEN2/4d30
US-10-719-547-18

Query Match      89.3%; Score 25; DB 21; Length 10616;
Best Local Similarity 89.3%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCMTCAATCCCTGCTGTTGG 28
   ||||| ||||| ||||| ||||| |||||
Db 304 CCCATCTCTCAGTAATCCCTGCTGTTGG 277

RESULT 3
US-10-719-547-14/c
; Sequence 14, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9, 13, 14
; OTHER INFORMATION: n = inosine
US-10-085-944-1

Query Match      89.3%; Score 25; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCATCTCMTCAATCCCTGCTGTTGG 28
   ||||| ||||| ||||| ||||| |||||
Db 1 CCCATCTCMTCAATCCCTGCTGTTGG 28

RESULT 2
US-10-719-547-16/c
; Sequence 16, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Recombinant Dengue 4 virus strain rDEN4
US-10-719-547-16

Query Match      89.3%; Score 25; DB 21; Length 10649;
Best Local Similarity 89.3%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCMTCAATCCCTGCTGTTGG 28
   ||||| ||||| ||||| ||||| |||||
Db 306 CCCATCTCTCAGTAATCCCTGCTGTTGG 279

RESULT 4
US-10-719-547-14
; Sequence 14, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
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; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10724
; TYPE: DNA
; ORGANISM: Dengue virus type 2
; US-10-699-550-4

Query Match      89.3%; Score 25; DB 19; Length 10724;
Best Local Similarity 89.3%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
Db 304 CCCATCTCTTCAGTATCCCTGCTGTTGG 277

RESULT 6
US-10-247-960-2/c
; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; FILE REFERENCE: 24733-20005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

Query Match      77.9%; Score 21.8; DB 16; Length 3381;
Best Local Similarity 82.1%; Pred. No. 3.4;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTTGG 181

RESULT 7
US-10-871-775-30/c
; Sequence 30, Application US/10871775
; Publication No. US20050100886A1
; GENERAL INFORMATION:
; APPLICANT: Pletnev, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND

; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US03/00594
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,281
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dengue2 (Tonga/74) plasmid p2
US-10-871-775-30

Query Match      77.9%; Score 21.8; DB 21; Length 15159;
Best Local Similarity 82.1%; Pred. No. 3.9;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
Db 304 CCCATCTTTTAAATATCCCTGCTGTTGG 277

RESULT 8
US-10-699-550-3/c
; Sequence 3, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10735
; TYPE: DNA
; ORGANISM: Dengue virus type 1
US-10-699-550-3

Query Match      72.1%; Score 20.2; DB 19; Length 10735;
Best Local Similarity 78.6%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
Db 302 CCCATCTAGCCAAATTCCTGCTGTTGG 275

RESULT 9
US-10-425-115-162694/c
; Sequence 162694, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 162694
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_79953C.1
US-10-425-115-162694

Query Match      68.6%; Score 19.2; DB 20; Length 422;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2  CCATCTCCTCANNATCCCTGCTGTG 28
Db      338 CCATCTCCGAGGTTCCCTGCTGTG 312

RESULT 10
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

Query Match      68.6%; Score 19.2; DB 13; Length 691;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1  CCCATCTCCTCANNATCCCTGCTGTG 27
Db      562 CCAGCTCCTCATGTTCCCTGCTGTG 536

RESULT 11
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

Query Match      68.6%; Score 19.2; DB 22; Length 52746;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1  CCCATCTCCTCANNATCCCTGCTGTG 27
Db      49957 CCACCTCCACAGCATCCCTGCTGTG 49983

RESULT 12
US-10-737-082-39
; Sequence 39, Application US/10737082
; Publication No. US20050130170A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Beard, Chris
; APPLICANT: Burgess, Chris
; APPLICANT: Gannon, Allison
; APPLICANT: Harvey, Jeanne
; APPLICANT: Lechner, John F.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
; FILE REFERENCE: 1657/2032
; CURRENT APPLICATION NUMBER: US/10/737,082
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 10/737,082
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 300
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 52746
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-082-39

Query Match      68.6%; Score 19.2; DB 22; Length 52746;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1  CCCATCTCCTCANNATCCCTGCTGTG 27
Db      49957 CCACCTCCACAGCATCCCTGCTGTG 49983
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RESULT 13
US-10-765-790-39
; Sequence 39, Application US/10765790
; Publication No. US20050130172A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Beard, Chris
; APPLICANT: Burgess, Chris
; APPLICANT: Gannon, Allison
; APPLICANT: Harvey, Jeanne
; APPLICANT: Lechner, John F.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
; FILE REFERENCE: 1657/2035
; CURRENT APPLICATION NUMBER: US/10/765,790
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 10/737,082
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 300
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 52746
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-39

Query Match      68.6%; Score 19.2; DB 22; Length 52746;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGG 27
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Db 49957 CCCACTCCACAGCATCCAGCTGTTG 49983

RESULT 14
US-10-437-963-62174/c
; Sequence 62174, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 62174
; LENGTH: 2739
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_63534C.1
US-10-437-963-62174

Query Match      67.1%; Score 18.8; DB 19; Length 2739;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATCTCTCANNATCCCTGCTGTTGG 28
    ||||| ||||| ||||| ||||| |||||
Db 2585 ATATCTTCAGTATCCCTGCTGATGG 2561

RESULT 15
US-10-029-386-27304
```

```
; Sequence 27304, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27304
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUE 9.00e-73
; OTHER INFORMATION: EST_HUMAN HIT: AA160611.1, EVALUE 4.00e-76
; OTHER INFORMATION: NT HIT: AF251442.1, EVALUE 0.00e+00
US-10-029-386-27304

Query Match      66.4%; Score 18.6; DB 16; Length 482;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
    ||||| ||||| ||||| ||||| |||||
Db 50 CCCATCTCTCATACTCACTGTTGCTGG 77

RESULT 16
US-09-864-761-27448/c
; Sequence 27448, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 27448
;; LENGTH: 486
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004816.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.92
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.88
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: NT HIT: U07747.1, EVALUE 1.00e-15
;; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUE 8.00e-73
;; OTHER INFORMATION: EST_HUMAN HIT: AA160611.1, EVALUE 3.00e-76
US-09-864-761-27448

Query Match 66.4%; Score 18.6; DB 9; Length 486;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
|||||
DB 433 CCCATCTCTTCATCTACTCAGTGTGCTGG 406

RESULT 17
US-10-029-386-13604
;; Sequence 13604, Application US/10029386
;; Publication No. US20030194704A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Hanzel, David K.
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: ABOMICA-X-2
;; CURRENT APPLICATION NUMBER: US/10/029,386
;; CURRENT FILING DATE: 2001-12-20
;; NUMBER OF SEQ ID NOS: 34288
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 13604
;; LENGTH: 577
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO CHR14.3
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
;; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUE 1.00e-72
;; OTHER INFORMATION: NT HIT: g14749516, EVALUE 0.00e+00
;; OTHER INFORMATION: EST_HUMAN HIT: AA160611.1, EVALUE 5.00e-76
US-10-029-386-13604

Query Match 66.4%; Score 18.6; DB 16; Length 577;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
|||||
DB 93 CCCATCTCTTCATCTACTCAGTGTGCTGG 120

RESULT 18
US-10-437-963-53513/c
;; Sequence 53513, Application US/10437963
;; Publication No. US20040123343A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Wu, Wei
;; APPLICANT: Boukharov, Andrey A.
;; APPLICANT: Barbazuk, Brad
;; APPLICANT: Li, Ping
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 53513
;; LENGTH: 2301
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_55706C.1
US-10-437-963-53513

Query Match 66.4%; Score 18.6; DB 19; Length 2301;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
|||||
DB 1933 CCCATCTCTTCATGATGATGATGATGATGATG 1906

RESULT 19
US-10-322-281-484/c
;; Sequence 484, Application US/10322281
;; Publication No. US20040126762A1
;; GENERAL INFORMATION:
;; APPLICANT: David W. Morris
;; APPLICANT: Marc S. Malandro
;; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;; FILE REFERENCE: 529452001000
;; CURRENT APPLICATION NUMBER: US/10/322,281
;; CURRENT FILING DATE: 2002-12-17
;; NUMBER OF SEQ ID NOS: 866
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 484
;; LENGTH: 6412
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-322-281-484

Query Match 66.4%; Score 18.6; DB 19; Length 6412;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
|||||
DB 1558 CCCCACTCTCTCACTCTCCCTGCTGATGG 1531

RESULT 20
US-10-322-281-483/c
;; Sequence 483, Application US/10322281
;; Publication No. US20040126762A1
;; GENERAL INFORMATION:
;; APPLICANT: David W. Morris
;; APPLICANT: Marc S. Malandro


```

; PRIOR APPLICATION NUMBER: PCT/US99/24331
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,737
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-918-897-12

Query Match      65.0%; Score 18.2; DB 21; Length 2385;
Best Local Similarity 76.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCTTCCTGCTGTT 26
Db 1590 CCCCTCTCCTCAGTCTTCCTGCTGTT 1565

RESULT 28
US-09-759-143-333/c
; Sequence 333, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-333

Query Match      65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCTTCCTGCTGTT 26
Db 1455 CCCCTCTCCTCAGTCTTCCTGCTGTT 1430

RESULT 30
US-09-822-827-333/c
; Sequence 333, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-333

Query Match      65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCTTCCTGCTGTT 26
Db 1455 CCCCTCTCCTCAGTCTTCCTGCTGTT 1430

RESULT 31
US-09-232-880-333/c
; Sequence 333, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
```


; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTT 26
Db 1455 CCCTCTCTCTCAGTCTTCTGCTGTT 1430

RESULT 32
US-09-895-793-333/c
; Sequence 333, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTT 26
Db 1455 CCCTCTCTCTCAGTCTTCTGCTGTT 1430

RESULT 33
US-09-895-814-333/c
; Sequence 333, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTT 26
Db 1455 CCCTCTCTCTCAGTCTTCTGCTGTT 1430

RESULT 34
US-10-012-896-333/c
; Sequence 333, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.

RESULT 38

US-10-318-389-4/c
; Sequence 4, Application US/10318389
; Publication No. US20040121328A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF PHOSPHODIESTERASE 8A EXPRESSION
; FILE REFERENCE: PFS-0062
; CURRENT APPLICATION NUMBER: US/10/318,389
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 4
; LENGTH: 77777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2937..3926
; OTHER INFORMATION: n = A,T,C or G
US-10-318-389-4

Query Match 65.0%; Score 18.2; DB 19; Length 77777;
Best Local Similarity 76.9%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCATCTCNCANNATCCCTGCTGTT 26

Db 11216 CCACCCCTCAACATCCCTGCTTT 11191

RESULT 39

US-10-175-523-197
; Sequence 197, Application US/10175523
; Publication No. US2003009264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/1J795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 81826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(81826)
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown, or other
US-10-175-523-197

Query Match 65.0%; Score 18.2; DB 14; Length 81826;
Best Local Similarity 76.9%; Pred. No. 2.3e+02;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCATCTCNCANNATCCCTGCTGTTG 27
Db 44815 CCATCACTTCACCAACGCTGCTGTTG 44840

RESULT 40

US-10-719-993-7053/c
; Sequence 7053, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7053
; LENGTH: 117985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-7053

Query Match 65.0%; Score 18.2; DB 20; Length 117985;
Best Local Similarity 76.9%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCATCTCNCANNATCCCTGCTGTTG 27

Db 79562 CCATCTCATCTGTTTACCTGCTGTTG 79537

Search completed: July 31, 2005, 15:45:50
Job time : 351.5 secs

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 10:46:20 ; Search time 818 Seconds
(without alignments)
1658.614 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatagtctgaacgcgagagaaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	100.0	342	14	FLD2CPW2
2	28	100.0	840	14	AF360860
3	28	100.0	840	14	AF360861
4	28	100.0	840	14	AF360862
5	28	100.0	840	14	AF360863
6	28	100.0	2319	14	S66064
7	28	100.0	2325	14	AF469175
8	28	100.0	2325	14	AF469176
9	28	100.0	2325	14	AF509530
10	28	100.0	2325	14	AY044442
11	28	100.0	2357	6	AR232496
12	28	100.0	2357	14	DEN2NGC
13	28	100.0	2469	14	DENJAMA
14	28	100.0	2552	14	AY152036S1
15	28	100.0	2552	14	AY152040S1
16	28	100.0	2552	14	AY152044S1
17	28	100.0	2552	14	AY152048S1
18	28	100.0	2552	14	AY152052S1
19	28	100.0	2552	14	AY152056S1

20	28	100.0	2552	14	AY152060S1	AY152060 Dengue vi
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28	28	100.0	2552	14	AY152092S1	AY152092 Dengue vi
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32	28	100.0	2552	14	AY152108S1	AY152108 Dengue vi
33	28	100.0	2552	14	AY152112S1	AY152112 Dengue vi
34	28	100.0	2552	14	AY152116S1	AY152116 Dengue vi
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243	26.4	94.3	10735	14	AF514885	Dengue vi	316	23.2	82.9	1050	14	AB010984	Dengue vi
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247	26.4	94.3	10735	14	AY277665	Dengue vi	320	23.2	82.9	1050	14	AB010988	Dengue vi
248	26.4	94.3	10735	14	AY277666	Dengue vi	321	23.2	82.9	1050	14	AB010989	Dengue vi
249	26.4	94.3	10735	14	DVU88535	Dengue vi	322	23.2	82.9	1050	14	AB010990	Dengue vi
250	26.4	94.3	10735	14	DVU88536	Dengue vi	323	22.2	79.3	240609	2	CR387997	Danio rer
251	26.4	94.3	10735	14	DVU88537	Dengue vi	324	22	78.6	72	6	AX573313	Sequence
252	26	92.9	26	6	AX042245	Sequence	325	21.6	77.1	3361	14	DVU88237	Dengue vi
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254	24.8	88.6	318	14	AF495890	Dengue vi	327	20.4	72.9	62381	5	BX640594	Zebrafish
255	24.8	88.6	318	14	AF495892	Dengue vi	328	20.4	72.9	191426	2	BX927352	Danio rer
256	24.8	88.6	318	14	AF495893	Dengue vi	329	20	71.4	11064	14	AY453412	Ueutu vir
257	24.8	88.6	318	14	AF495894	Dengue vi	330	20	71.4	11066	14	AY453411	Ueutu vir
258	24.8	88.6	318	14	AF495896	Dengue vi	331	20	71.4	302050	1	AP006568	Gloeobact
259	24.8	88.6	318	14	AF495897	Dengue vi	332	19.6	70.0	110000	8	CR380953	Continuation (8 of
260	24.8	88.6	318	14	AF495898	Dengue vi	333	19.6	70.0	154341	5	CR381651	Zebrafish
261	24.8	88.6	318	14	AF495899	Dengue vi	334	19.6	70.0	187708	2	CR788293	Danio rer
262	24.8	88.6	318	14	AF495901	Dengue vi	335	19.6	70.0	209785	2	AC109497	Mus muscu
263	24.8	88.6	318	14	AF495903	Dengue vi	336	19.2	68.6	1081	8	AY085057	Arabidops
264	24.8	88.6	318	14	AF495904	Dengue vi	337	19.2	68.6	1920	8	YSP2FS	Arabidops
265	24.8	88.6	318	14	AF495905	Dengue vi	338	19.2	68.6	18991	8	SPBC1718	Schizosacch
266	24.8	88.6	318	14	AF495906	Dengue vi	339	19.2	68.6	66303	9	BX470173	Human DNA
267	24.8	88.6	495	14	AF008555	Dengue vi	340	19.2	68.6	80167	8	AB022216	Arabidops
268	24.8	88.6	1050	14	AB038465	Dengue vi	341	19.2	68.6	144648	9	AL391832	Human DNA
269	24.8	88.6	1050	14	AB038466	Dengue vi	342	19.2	68.6	172138	2	AC064796	Homo sapi
270	24.8	88.6	1050	14	AB038467	Dengue vi	343	19.2	68.6	209384	2	AC016618	Homo sapi
271	24.8	88.6	1050	14	AB038468	Dengue vi	344	19.2	68.6	237669	2	AC146821	Otolenur
272	24.8	88.6	1050	14	AB038469	Dengue vi	345	19	67.9	19	6	CQ789608	Sequence
273	24.8	88.6	1050	14	AB038470	Dengue vi	346	19	67.9	110000	2	AP006493	Continuation (2 of
274	24.8	88.6	1050	14	AB038471	Dengue vi	347	19	67.9	130130	2	AC117804	Mus muscu
275	24.8	88.6	1050	14	AB038472	Dengue vi	348	19	67.9	144319	9	AC007968	Homo sapi
276	24.8	88.6	1050	14	AB038473	Dengue vi	349	19	67.9	165158	2	AC141687	Apis mell
277	24.8	88.6	1050	14	AB038474	Dengue vi	350	19	67.9	166490	9	AL359438	Human DNA
278	24.8	88.6	1050	14	AB038475	Dengue vi	351	19	67.9	169243	2	BX510323	Danio rer
279	24.8	88.6	1050	14	AB038476	Dengue vi	352	19	67.9	178426	10	AL928631	Mouse DNA
280	24.8	88.6	1050	14	AB038477	Dengue vi	353	19	67.9	209319	2	AC107799	Mus muscu
281	24.8	88.6	1050	14	AB038478	Dengue vi	354	19	67.9	215505	10	AL844166	Mouse DNA
282	24.8	88.6	1050	14	AB038479	Dengue vi	355	19	67.9	219405	6	AC118096	Rattus no
283	24.8	88.6	2297	14	DENENVAA	Dengue vi	356	19	67.9	227871	2	AC132915	Mus muscu
284	24.8	88.6	2880	14	AY099338S1	Dengue vi	357	19	67.9	243627	2	AC122962	Rattus no
285	24.8	88.6	2880	14	AY099339S1	Dengue vi	358	19	67.9	270916	9	AC135523	Rattus no
286	24.8	88.6	2880	14	AY099340S1	Dengue vi	359	18.8	67.1	56051	2	AC010177	Homo sapi
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288	24.8	88.6	2880	14	AY099342S1	Dengue vi	361	18.6	66.4	1145	6	AR504859	Sequence
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290	24.8	88.6	3000	14	DENSP5AA	Dengue vi	363	18.6	66.4	2950	3	BT011150	Drosophil
291	24.8	88.6	10696	14	AF317645	Dengue vi	364	18.6	66.4	3002	6	CQ614256	Sequence
292	24.8	88.6	10696	14	DENCM6	Dengue type	365	18.6	66.4	7264	6	CQ614255	Sequence
293	24.8	88.6	10699	6	AX224227	Sequence	366	18.6	66.4	8247	1	AB006036	Pasteurel
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295	24.8	88.6	10703	14	AB1679147	Dengue vi	368	18.6	66.4	18788	1	AY271621	Pseudomna
296	24.8	88.6	10707	14	AB1891125	Dengue vi	369	18.6	66.4	34733	3	CED2089	Caenorhabdi
297	24.8	88.6	10707	14	AB1891126	Dengue vi	370	18.6	66.4	48744	2	AC014368	Drosophil
298	24.8	88.6	10707	14	AB1891127	Dengue vi	371	18.6	66.4	64168	4	AY152834	Felis cat
299	24.8	88.6	10707	14	AB1891128	Dengue vi	372	18.6	66.4	85338	3	AC004279	Drosophil
300	24.8	88.6	10707	14	AY099336	Dengue vi	373	18.6	66.4	93121	2	DMR48A1	Drosophil
301	24.8	88.6	10707	14	AY099337	Dengue vi	374	18.6	66.4	100248	2	AC013150	Drosophil
302	24.8	88.6	10707	14	AY648961	Dengue vi	375	18.6	66.4	110000	2	AC128221	Continuation (2 of
303	24.8	88.6	10707	14	AY662691	Dengue vi	376	18.6	66.4	112895	9	AC107210	Homo sapi
304	24.8	88.6	10735	14	AY277664	Dengue vi	377	18.6	66.4	124456	2	AC017830	Drosophil
305	24.8	88.6	15145	12	AY656170	Dengue vi	378	18.6	66.4	145952	3	AB003675	Drosophil
306	24.8	88.6	15176	12	AY656169	Dengue vi	379	18.6	66.4	159862	2	CR788253	Danio rer
307	23.8	85.0	318	14	AF495900	Dengue vi	380	18.6	66.4	161579	3	AC010212	Drosophil
308	23.4	83.6	501	14	AF538025	Dengue vi	381	18.6	66.4	162239	2	AC079086	Homo sapi
309	23.4	83.6	501	14	AF538026	Dengue vi	382	18.6	66.4	167912	3	AC007650	Drosophil
310	23.2	82.9	318	14	AF495889	Dengue vi	383	18.6	66.4	173380	3	AC099011	Drosophil
311	23.2	82.9	318	14	AF495891	Dengue vi	384	18.6	66.4	177199	5	BX547933	Zebrafish

Department of Genetics and Cellular Biology, 5910 Kuala Lumpur, Malaysia
See <M15075> and <M19197> for previously reported sequence. See <X51708> and <X51710> for capsid protein sequences of M1 and M3.
Location/Qualifiers
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 40 AATATGCTGAACCGCGAGAGAACCGCG 67
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RESULT 2
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LOCUS
DEFINITION
Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.
ACCESSION
AF360860
VERSION
AF360860.1 GI:18644121
KEYWORDS
SOURCE
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 840)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
11714970
2 (bases 1 to 840)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
Direct Submission
Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England
Location/Qualifiers
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FEATURES
source

LOCUS AF360862 840 bp ss-RNA linear VRL 11-FEB-2002
DEFINITION Dengue virus type 2 isolate LARD1910 polyprotein gene, partial cds.
ACCESSION AF360862
VERSION AF360862.1 GI:18644125
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 840)
AUTHORS Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
JOURNAL 21571640
MEDLINE
PUBMED 11714970
REFERENCE
2 (bases 1 to 840)
AUTHORS Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 840;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAACCGCG 28
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RESULT 5
AF360863
LOCUS AF360863 840 bp ss-RNA linear VRL 11-FEB-2002
DEFINITION Dengue virus type 2 isolate LARD1996 polyprotein gene, partial cds.
ACCESSION AF360863
VERSION AF360863.1 GI:18644127
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 840)
AUTHORS Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
JOURNAL 21571640
MEDLINE
PUBMED 11714970

REFERENCE
2 (bases 1 to 840)
AUTHORS Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England
FEATURES
Location/Qualifiers
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/db_xref="GI:18644128"
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DTITYKCPLLRQNEPIDWCNSTSTWVTYGTCTTTGHRREKRSVALVPHVGMGLE
TRTETWMSSEGAMKHVQRIETWILRHGFAIMAILAYTIGTTHFQALIFILLTAVA
PSMT"
ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 840;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAACCGCG 28
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Db 40 AATATGCTGAACCGGAGAGAACCGCG 67
RESULT 6
S66064
LOCUS S66064 2319 bp DNA linear VRL 04-DEC-1993
DEFINITION structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
2319 nt].
ACCESSION S66064
VERSION S66064.1 GI:432575
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 4
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2319)
AUTHORS Kawano,H., Rostapehrov,V., Rosen,L. and Lai,C.J.
TITLE Genetic determinants of dengue type 4 virus neurovirulence for mice
J. Virol. 67 (11), 6567-6575 (1993)
JOURNAL 94016840
MEDLINE
PUBMED 8411360
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138430] from the original journal article.
FEATURES
Location/Qualifiers
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/db_xref="taxon:11070"
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TTTYECPLLVNTEPIDWCNLTSAWVNYGTCTQSGERRRKRKSVALTTPHSGMGLT

RAETWMSSEGAKWAQVRSWILRNPFPALLAGFMAYMIGOTGIQRTVFVLMMLVAP
SYGRCVGNRRDFVSGSGAWDSVLEHGGCVTTMAQCKPFLDELKTRAKEVAL
LRTYEASISNITATRCPTQGEYKBEQDOYICRDVDVDRGWNGCGPGRKGV
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EVKLPDYGELTDCBPSRGIDFENMILMKMKKTWLHVHKQWFLDLPLPMAAGADTSEV
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Indels 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64
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RESULT 7

AF469175

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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REFERENCE

AUTHORS

TITLE

RESULT 9
AF509530
LOCUS AF509530 2325 bp RNA linear VRL 22-MAY-2002
DEFINITION Dengue virus type 2 polyprotein gene, partial cds.
ACCESSION AF509530
VERSION AF509530.1 GI:21070436
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
AUTHORS Ren, R., Yu, F., Dong, T., Wei, L., Hua, J., Yan, H. and Feng, C.
TITLE Isolation, identification and sequence analyses of dengue virus type 2 strain GD19/2001
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2325)
AUTHORS Ren, R., Yu, F., Dong, T., Wei, L., Hua, J., Yan, H. and Feng, C.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) Microbiology Department, The Military Medical Institute of Guangzhou Military District, Dongguanhuang Road, Guangzhou 510507, China
FEATURES
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/organism="Dengue virus type 2"
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/strain="GD19/2001"
/specific_host="dengue fever patient"
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/country="China: Guangdong province"
1. .>2325
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/db_xref="GI:21070437"
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DTIYKPLRQNEPDIQWCNSTSTWVTGCTTGEHRRKRSVALVPHVGMGLE
TRTETWSSSGAMHQAQRIETWLRHPGFTIMAVILATYITGTYFORVLPIILLTAVA
PSMTMRCIGISNRDVSFGSGSWDIVLEHSGSVTTMAKNKPTLDFELTKAKHPA
TLRKYCIEAKLTNTTASRPTQGEPSLNEEQDKRFCKHSMVDRGNGCGLFGKGG
IVTCAMFTCKNMKGKVVQNPENLYTIVTPHSGEENVVNDTGKCKEIKVTPQSSI
TEALTCGTVTMECSPTGLDNEMVLQNEKAMVLRQWFLDLPLPLPGAEVQ
SNWIKETLVTFKPHAKQDVVVLGSGEGAMHTALGATEIQMSSGNLLFTGHLKCR
LRMDKLQKMSYMCCTGKFKVKEIAETQHTIVIRVQVEGSGSPCKIPFEMDLK
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841. .2325
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAACCGCAGAGAAACCGCG 67
|||||

RESULT 10
AY044442
LOCUS AY044442 2325 bp ss-RNA linear VRL 10-FEB-2002
DEFINITION Dengue virus type 2 strain Maraz polyprotein gene, partial cds.
ACCESSION AY044442
VERSION AY044442.1 GI:18643733
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2325)

AUTHORS Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,
Holmes, E.C. and Gould, E.A.
TITLE Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
11714970
REFERENCE 2 (bases 1 to 2325)
AUTHORS Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.M.,
Holmes, E.C. and Gould, E.A.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Flavivirus Group, CEH-Oxford, Mansfield
Road, Oxford OX1 3SR, United Kingdom
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/country="Venezuela"
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TRTETWSSSGAMHQAQRIETWLRHPGFTIMAVILATYITGTYFORVLPIILLTAVA
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TLRKYCIEAKLTNTTASRPTQGEPSLNEEQDKRFCKHSMVDRGNGCGLFGKGG
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LRMDKLQKMSYMCCTGKFKVKEIAETQHTIVIRVQVEGSGSPCKIPFEMDLK
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841. .2325
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAACCGCAGAGAAACCGCG 67
|||||

RESULT 11
AR232496
LOCUS AR232496 2357 bp RNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6455509.
ACCESSION AR232496
VERSION AR232496.1 GI:27274633
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2357)
AUTHORS Kochel, T.J., Porter, K.R., Raviprakash, K., Hoffman, S.L. and
Hayes, C.C.
TITLE Dengue nucleic acid vaccines that induce neutralizing antibodies

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JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 60 AATATGCTGAACGCGAGAGAAACCGCG 87

RESULT 12
DEN2NGC 2357 bp RNA linear VRL 29-MAY-2002
LOCUS Dengue virus type 2 gene for polyprotein, partial cds, strain:New
DEFINITION Guinea C.
ACCESSION D00346
VERSION D00346.1 GI:221230
KEYWORDS Dengue virus type 2
SOURCE Dengue virus type 2
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 2357)
AUTHORS Gruenberg, A., Woo, W.S., Biedrzycka, A. and Wright, P.J.
TITLE Partial nucleotide sequence and deduced amino acid sequence of the
structural proteins of dengue virus type 2, New Guinea C and
PUO-218 strains
JOURNAL J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
MEDLINE 88259474
PUBMED 3385407
COMMENT Nucleotide 1 in the NCG sequence corresponds to nucleotide 77
counting from the 5' end of the DEN-2(JAM) sequence.
FEATURES
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    /mol_type="genomic RNA"
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    TRTETWMSSEGAWKQVRIETWILRHFGFTIMAAIAYTIGTHFORALIFILLTAVA
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    TLKVCIEAKLTNTTDSRCTQGPESLNEEDKRFVCKHSMVDRGNGCGLFGKGG
    IVTCAMFTCKKMGKVLPENLEYTIVTPHSGEHAHVNDTGKHGKIKITPQSSI
    TEAELTYGVTMECSPTGLDNEMLVQLQMEDEKAWLVHROFPLDLPWLPQADTQG
    SNWIKETLVTFNPHAKQDVVVLGSGQEGAMHTALTGATEIQMSGNLLFTGHLKCR
    LRMDLQLKMSYVSMCTGKPVVKEIAETQGTIVIRVQYEGDGPCKIPFEIMDLK
    RHLVGLRLITVNPITVEKSPVNIETAEPPFGDSYIIIGVBPGLKLNWFKKSGSIGOMI
    ETTMRGAKMALIGDAMDGSLGGVFTSIGKALHGVFGAIYGAAFSGVSWTKILIG
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JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
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    /mol_type="genomic RNA"

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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 60 AATATGCTGAACGCGAGAGAAACCGCG 87

RESULT 13
DENJAMA 2469 bp ss-RNA linear VRL 18-MAR-2002
LOCUS Dengue virus type 2 ARAC 8110827 polyprotein gene, partial cds.
DEFINITION M15075
ACCESSION M15075.1 GI:323650
KEYWORDS Dengue virus type 2
SOURCE Dengue virus type 2
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 2469)
AUTHORS Deubel, V., Kinney, R.M. and Trent, D.W.
TITLE Nucleotide sequence and deduced amino acid sequence of the
structural proteins of dengue type 2 virus, Jamaica genotype
Virology 155 (2), 365-377 (1986)
JOURNAL 87071658
MEDLINE 3024394
PUBMED
FEATURES
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    TLKVCIEAKLTNTTDSRCTQGPESLNEEDKRFVCKHSMVDRGNGCGLFGKGG
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    LRMDLQLKMSYVSMCTGKPVVKEIAETQGTIVIRVQYEGDGPCKIPFEIMDLK
    RHLVGLRLITVNPITVEKSPVNIETAEPPFGDSYIIIGVBPGLKLNWFKKSGSIGOMI
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JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2469;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db 136 AATATGCTGAACCGGAGAGAACCGCG 163
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RESULT 14
AY152036S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152036
VERSION AY152036.1 GI:28170806
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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1. .2552
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VERSION AY152044.1 GI:28170824
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SOURCE
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Dengue virus type 4 (DEN-4)
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DEFINITION Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial cds.
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ORGANISM
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
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Flavivirus; Dengue virus group.
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Dengue virus type 4 (DEN-4)
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ORGANISM Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
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TITLE Direct Submission
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Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ACCESSION AV152048
VERSION AV152048.1 GI:28170833
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Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus

ORGANISM Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
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REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus

JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
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Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Dengue virus type 4 (DEN-4)
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Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

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	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,									
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 21
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DEFINITION Dengue virus type 4 D4.47_1998 polyprotein precursor, gene, partial
cds.
ACCESSION AY152064
VERSION AY152064.1 GI:28170869
KEYWORDS
SEGMENT
SOURCE
ORGANISM
REFERENCE 1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beitran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beitran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
FEATURES source
1. .>2552
/organism="Dengue virus type 4"
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LVLWIGTNRGNTSMATCIAGVGITILFLGTQVADMGCVVSNWSGRELKCSARIPVDND
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 22
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DEFINITION Dengue virus type 4 D4.13_1998 polyprotein precursor, gene, partial
cds.
ACCESSION AY152068
VERSION AY152068.1 GI:28170878
KEYWORDS
SEGMENT
SOURCE
ORGANISM
REFERENCE 1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beitran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beitran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
FEATURES source
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.14;

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Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28

Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 23

AY152072S1

LOCUS

DEFINITION Dengue virus type 4 D4.46_1998 polyprotein precursor, gene, partial cds.

ACCESSION

AY152072

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

i of 4

Dengue virus type 4 (DEN-4)

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

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ORIGIN

Query Match

Best Local Similarity 100.0%; Score 28; DB 14; Length 2552;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches

Qy

Db

RESULT 24

AY152076S1

LOCUS

DEFINITION

AY152076

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

i of 4

Dengue virus type 4 (DEN-4)

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Score 28; DB 14; Length 2552;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

Db

RESULT 24

AY152076S1

LOCUS

DEFINITION

AY152076

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

i of 4

Dengue virus type 4 (DEN-4)

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

source

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RESULT 25
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LOCUS              D4.15_1998 polyprotein precursor, gene, partial
DEFINITION
cds.

ACCESSION          AY152080
VERSION            GI:28170905
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltzan,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE
JOURNAL
PUBMED
12832629
2 (bases 1 to 2552)
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; serNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltzan,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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ORIGIN
Query Match      100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAACCGCG 28
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DB 37 AATATGCTGAACCGCAGAGAAACCGCG 64

RESULT 26
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LOCUS              D4.4_1994 polyprotein precursor, gene, partial
DEFINITION
cds.

ACCESSION          AY152084
VERSION            GI:28170914
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltzan,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE
JOURNAL
PUBMED
12832629
2 (bases 1 to 2552)
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; serNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltzan,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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AUTHORS      Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE        Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL      Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED      12832629
REFERENCE    2 (bases 1 to 2552)
AUTHORS      Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE        Direct Submission
JOURNAL      Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
              Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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              EVKLPDPELTLDCEPRSGIDFNEMILMKMKKTLVHKQWFLDLPWPWTAGADTSEV
              HWNYKERMVTFKVPKAKQDVTVLGSQEGAMHSALAGATEVSDGDNHMFAGHLCKV
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              KTVGRVISTPLAENTVNIELEPPFGDSYIVIGVNSALTLLHWFRKGSIGKMF
              STYRGAKRMALIGTAMDGFSVGLFTSLGKAVHOVFGSVYTTMFGVGSWMIRLIGF
              LVLWIGTNSRNTSMAMTCIAGVGITLFLGTVOADMGCVVWSGRELKCGSGIFVVDN
              VHTWTEQYKQPESPARLASAILNAHKDGVCGIRSTRTLENVVMWKQITNELN"
ORIGIN
Query Match      100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
    |||||
Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 29
AY152096S1
LOCUS      Dengue virus type 4 D4.113_1995VE polyprotein precursor, gene, partial
DEFINITION
cgs.
ACCESSION  AY152096
VERSION     AY152096.1 GI:28170941
KEYWORDS    1 of 4
SEGMENT     Dengue virus type 4 (DEN-4)
SOURCE      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
              Flavivirus; Dengue virus group.
REFERENCE    1 (bases 1 to 2552)
AUTHORS      Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
              Selection-Driven Evolution of Emergent Dengue Virus
              Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
              12832629
              2 (bases 1 to 2552)
              Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
              Direct Submission
              Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
              Piedras, PO Box 23360, San Juan 00931, Puerto Rico
              Location/Qualifiers
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 28
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LOCUS      Dengue virus type 4 D4.113_1995VE polyprotein precursor, gene,
DEFINITION
partial cds.
ACCESSION  AY152092
VERSION     AY152092.1 GI:28170932
KEYWORDS    1 of 4
SEGMENT     Dengue virus type 4 (DEN-4)
SOURCE      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE    1 (bases 1 to 2552)
AUTHORS      Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
              Selection-Driven Evolution of Emergent Dengue Virus
              Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
              12832629
              2 (bases 1 to 2552)
              Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
              Direct Submission
              Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
              Piedras, PO Box 23360, San Juan 00931, Puerto Rico
              Location/Qualifiers
              1. .2552
              /organism="Dengue virus type 4"

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 29
AY152096S1
LOCUS      Dengue virus type 4 D4.113_1994 polyprotein precursor, gene, partial
DEFINITION
cgs.
ACCESSION  AY152096
VERSION     AY152096.1 GI:28170941
KEYWORDS    1 of 4
SEGMENT     Dengue virus type 4 (DEN-4)
SOURCE      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
              Flavivirus; Dengue virus group.
REFERENCE    1 (bases 1 to 2552)
AUTHORS      Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
              Selection-Driven Evolution of Emergent Dengue Virus
              Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
              12832629
              2 (bases 1 to 2552)
              Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
              Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
              Direct Submission
              Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
              Piedras, PO Box 23360, San Juan 00931, Puerto Rico
              Location/Qualifiers
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ORIGIN
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Query Match      100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AATATGCTGAACCGCAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGCAGAGAAACCGCG 64
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RESULT 32
LOCUS AY152108S1
DEFINITION Dengue virus type 4 D4.3_1987 polyprotein precursor, gene, partial cds.
ACCESSION AY152108
VERSION AY152108.1 GI:28170968
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1. of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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ORIGIN
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RESULT 32
LOCUS AY152108S1
DEFINITION Dengue virus type 4 D4.3_1987 polyprotein precursor, gene, partial cds.
ACCESSION AY152108
VERSION AY152108.1 GI:28170968
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1. of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
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RESULT 32
LOCUS AY152108S1
DEFINITION Dengue virus type 4 D4.3_1987 polyprotein precursor, gene, partial cds.
ACCESSION AY152108
VERSION AY152108.1 GI:28170968
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1. of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
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/notes="contains core protein, matrix protein and envelope
glycoprotein"
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ORIGIN
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ORIGIN
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ORIGIN

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Query Match      100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGG 28
|||||
Db 37 AATATGCTGAACCGGAGAGAAACCGG 64

RESULT 34
AY152116S1          2552 bp      RNA      linear      VRL 29-SEP-2003
LOCUS              Dengue virus type 4 D4.86_1994 polyprotein precursor, gene, partial
DEFINITION
ACCESSION          AY152116      GI:28170986
VERSION            1
KEYWORDS
SEGMENTS
SOURCE
ORGANISM
REFERENCE
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
LOCATION/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS              Dengue virus type 4 D4.80_1994 polyprotein precursor, gene, partial
DEFINITION
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DEFINITION
ACCESSION          AY152120      GI:28170995
VERSION            1
KEYWORDS
SEGMENTS
SOURCE
ORGANISM
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
LOCATION/Qualifiers
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Query Match      100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGG 64

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LOCUS              Dengue virus type 4 D4.80_1994 polyprotein precursor, gene, partial
DEFINITION
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12832629

2 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

Location/Qualifiers

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/organism="Dengue virus type 4"

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Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AY152136S1

LOCUS

DEFINITION

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Dengue virus type 4 D4.76_1994 polyprotein precursor, gene, partial cds.

ACCESSION

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

1 of 4

Dengue virus type 4 (DEN-4)

Dengue virus type 4

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

2 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

JOURNAL

FEATURES
source

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ORIGIN

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ACCESSION
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Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64
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Search completed: July 31, 2005, 12:50:16
Job time : 831 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:03:16 ; Search time 214 Seconds
(without alignments)
774.546 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 atatacgtgaacgcgcagagaaacccgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

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7: Geneseqn2002bs:*

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11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	28	100.0	2423	12	ADG93319 Dengue vi
5	28	100.0	3381	2	AAT47666 Dengue vi
6	28	100.0	3381	2	AAX25114 Dengue vi
7	28	100.0	3381	11	ADL98085 Dengue vi
8	28	100.0	3381	12	ADQ28715 Dengue vi
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25	26.4	94.3	2426	12	ADG93317	Adg93317 DEN1 (Pue
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C 69	18.4	65.7	11313	12	ADP86269	Adp86269 Hepatitis
C 70	18.4	65.7	11313	12	ADP86275	Adp86275 Hepatitis
C 71	18.4	65.7	11313	12	ADP86267	Adp86267 Hepatitis
C 72	18.4	65.7	12306	10	ADI41414	Adi41414 BB7 nucle
C 73	18.4	65.7	12315	10	ADI41413	Adi41413 BB7M4HRLU
C 74	18.4	65.7	12980	2	AAV59364	Aav59364 Hepatitis
C 75	18.4	65.7	12980	6	ABX87286	Abx87286 Hepatitis
C 76	18.4	65.7	12980	8	ACA62469	Aca62469 DNA encod
C 77	18.4	65.7	15065	3	AAZ36195	Aaz36195 Nucleotid
C 78	18.4	65.7	16847	12	ADO07464	Ado07464 Japanese
79	18.4	65.7	18563	12	ADO07466	Ado07466 Japanese
80	18.4	65.7	18563	12	ADO07465	Ado07465 Japanese
81	18.4	65.7	18565	12	ADO07467	Ado07467 Japanese
82	18.4	65.7	19038	12	ADO07468	Ado07468 Japanese
83	18.4	65.7	19038	12	ADO07469	Ado07469 Japanese
84	18.4	65.7	19040	12	ADO07470	Ado07470 Japanese
85	18.2	65.0	333	4	AAI81993	Aai81993 Human pol
86	18.2	65.0	452	9	ACH40248	Ach40248 Human foe
87	18.2	65.0	2179	6	ABX34665	Abx34665 Human CDN
88	18.2	65.0	2617	12	ADQ62907	Adq62907 Novel hum
89	18.2	65.0	3017	2	AAZ75764	Aaz75764 Human gli
90	18.2	65.0	3030	13	ACN40225	Acn40225 Tumour-as
91	18.2	65.0	3033	10	ACC72810	Acc72810 Human can
92	18.2	65.0	3107	4	AAS75546	Aas75546 Human bra
93	18.2	65.0	6483	4	AAH57538	Aah57538 Human bra

c 94	18.2	65.0	9875	4	AAL05190	Aal05190 Human rep	c 167	17.2	61.4	1506	13	ADT42786	Adt42786 Bacterial
c 95	18	64.3	1716	5	AAS88884	Aas88884 DNA encod	168	17.2	61.4	1960	4	AAS60832	Aas60832 Human can
c 96	18	64.3	9636	4	AAK90449	Aak90449 Human dig	169	17.2	61.4	1960	5	ABV28961	Abv28961 Human pro
c 97	18	64.3	14952	10	ACF69283	Acf69283 Photorhab	170	17.2	61.4	1960	5	ABV28010	Abv28010 Human pro
c 98	18	64.3	100779	10	ACF65386 ⁶	Continuation (7 of	171	17.2	61.4	1960	5	ABV22171	Abv22171 Human pro
c 99	18	64.3	110000	10	ACF67367 ²²	Continuation (23 o	172	17.2	61.4	2270	4	ABL27934	AbL27934 Drosophil
c 100	17.8	63.6	973	4	AAI96919	Aai96919 Human neu	173	17.2	61.4	2300	4	ABL27932	AbL27932 Drosophil
c 101	17.8	63.6	4822	4	ABL20414	AbL20414 Drosophil	174	17.2	61.4	3201	13	ADR15119	Adr15119 Rat elect
c 102	17.6	62.9	550	11	ACN90669	Acn90669 Breast ca	175	17.2	61.4	3319	2	AAV43076	Aat43076 Wheat ace
c 103	17.6	62.9	557	4	AAI12137	Aai12137 Human bre	176	17.2	61.4	3319	2	AAV33412	Aatv33412 5' end fl
c 104	17.6	62.9	691	4	AAI21020	Aai21020 Human bre	177	17.2	61.4	24358	4	AAV33412	Aatv33412 5' end fl
c 105	17.6	62.9	694	3	AAZ53155	Aaz53155 Neisseria	178	17.2	61.4	417	8	ABX62329	Abx62329 Arabidops
c 106	17.6	62.9	695	3	AAZ53156	Aaz53156 Neisseria	179	17.2	61.4	435	11	ABD02565	Abd02565 Pseudomon
c 107	17.6	62.9	696	3	AAI15311	Aai15311 DNA encod	180	17.2	61.4	437	8	ABX37358	Abx37358 Bovine ES
c 108	17.6	62.9	838	11	ACN82318	Acn82318 Breast ca	181	17.2	61.4	473	6	ABN64425	Abn64425 Human can
c 109	17.6	62.9	945	6	ABQ69695	Abq69695 Listeria	182	17.2	61.4	1202	3	AAV37689	Aacv37689 Arabidops
c 110	17.6	62.9	945	6	ABQ69758	Abq69758 Listeria	183	17.2	61.4	1202	3	AAV44984	Aacv44984 Arabidops
c 111	17.6	62.9	966	6	ABQ67740	Abq67740 Listeria	184	17.2	61.4	1725	2	AAT60349	Aat60349 MAP kinas
c 112	17.6	62.9	966	6	ABQ67741	Abq67741 Listeria	185	17.2	61.4	1786	2	AAT60350	Aat60350 MAP kinas
c 113	17.6	62.9	1646	8	ACA41504	Aca41504 Prokaryot	186	17.2	61.4	1839	4	AAC90923	Aac90923 C. elegan
c 114	17.6	62.9	2485	12	ADO35406	Ado35406 Novel mou	187	17.2	61.4	1869	8	ADA68153	Ada68153 Arabidops
c 115	17.6	62.9	3363	13	ADR92364	Adr92364 Novel S.	188	17.2	61.4	1998	4	AAC90922	Aac90922 C. elegan
c 116	17.6	62.9	9718	2	AAT14180	Aat14180 Attenuate	189	17.2	61.4	2354	2	AAT36393	Aat36393 Lactococc
c 117	17.6	62.9	69936	3	AAAB1479	Aa81479 N. mening	190	17.2	61.4	2409	11	ABD02655	Abd02655 Pseudomon
c 118	17.6	62.9	84707	6	ABQ67196 ⁶	Continuation (7 of	191	17.2	61.4	3378	9	ADA32820	Ada32820 DNA encod
c 119	17.6	62.9	110000	3	AAAB1490 ⁰⁴	Continuation (5 of	192	17.2	61.4	6520	6	ABK83938	Abk83938 Human CDN
c 120	17.6	62.9	110000	6	ABQ67196 ¹	Continuation (2 of	193	17.2	61.4	14000	4	AAS46232	Aas46232 DNA encod
c 121	17.6	62.9	110000	6	ABQ69245 ²⁴	Continuation (25 of	194	17.2	61.4	163701	13	ABD33351	Abd33351 Murine ca
c 122	17.6	62.9	110000	6	ABQ69245 ²⁴	Continuation (27 o	195	16.8	60.0	69	12	ADN36694	Adn36694 West Nile
c 123	17.6	62.9	349980	3	AAF21607 ²⁶	Aaf21607 Neisseria	196	16.8	60.0	287	10	ABX82696	Abx82696 Corn ear-
c 124	17.4	62.1	356	5	AAF65359	Aaf65359 Novel hum	197	16.8	60.0	331	2	AAQ89698	Aaq89698 Transcrip
c 125	17.4	62.1	379	6	ABQ84757	Abq84757 Chlamydia	198	16.8	60.0	365	6	ABK51710	Abk51710 Partial c
c 126	17.4	62.1	379	6	ABQ78015	Abq78015 Chlamydia	199	16.8	60.0	366	8	ABQ76684	Abq76684 MNVcwt DN
c 127	17.4	62.1	379	8	ABX99182	Abx99182 C. psitta	200	16.8	60.0	503	6	ABQ31109	Abq31109 Oligonucl
c 128	17.4	62.1	589	6	ABQ47607	Abq47607 Oligonucl	201	16.8	60.0	503	6	ABQ31108	Abq31108 Oligonucl
c 129	17.4	62.1	589	6	ABQ47606	Abq47606 Oligonucl	202	16.8	60.0	509	6	ABQ20645	Abq20645 Oligonucl
c 130	17.4	62.1	657	2	AAQ03640	Aaq03640 Cucumbe	203	16.8	60.0	509	6	ABQ20644	Abq20644 Oligonucl
c 131	17.4	62.1	691	6	ABQ52041	Abq52041 Oligonucl	204	16.8	60.0	621	5	AAS29124	Aas29124 cDNA enco
c 132	17.4	62.1	691	6	ABQ52040	Abq52040 Oligonucl	205	16.8	60.0	621	6	ABS68264	Abs68264 cDNA enco
c 133	17.4	62.1	774	8	ACA51992	Aca51992 Prokaryot	206	16.8	60.0	621	10	ADC25258	Adc25258 Human CDN
c 134	17.4	62.1	778	8	ACA48879	Aca48879 Prokaryot	207	16.8	60.0	672	5	AAS68401	Aas68401 DNA encod
c 135	17.4	62.1	1227	9	ADA30601	Ada30601 DNA encod	208	16.8	60.0	681	10	ABZ38190	Abz38190 N. gonorr
c 136	17.4	62.1	1416	4	ABL07761	AbL07761 Drosophil	209	16.8	60.0	699	10	ADK55485	Adk55485 Plant DNA
c 137	17.4	62.1	2000	10	ACC61659	Acc61659 Gene sequ	210	16.8	60.0	716	6	ABQ40083	Abq40083 Oligonucl
c 138	17.4	62.1	2000	10	ADK64251	Adk64251 Disease t	211	16.8	60.0	716	6	ABQ40082	Abq40082 Oligonucl
c 139	17.4	62.1	2520	6	ABQ84758	Abq84758 Chlamydia	212	16.8	60.0	716	6	ABQ40081	Abq40081 Oligonucl
c 140	17.4	62.1	2520	6	ABQ78016	Abq78016 Chlamydia	213	16.8	60.0	788	6	ABQ20794	Abq20794 Oligonucl
c 141	17.4	62.1	2520	8	ABX99183	Abx99183 C. psitta	214	16.8	60.0	788	6	ABQ20795	Abq20795 Oligonucl
c 142	17.4	62.1	4017	4	ABL07760	AbL07760 Drosophil	215	16.8	60.0	857	6	ABQ43221	Abq43221 Oligonucl
c 143	17.4	62.1	5026	3	ABK64961	Aab64961 C. elegan	216	16.8	60.0	857	6	ABQ43220	Abq43220 Oligonucl
c 144	17.4	62.1	5026	3	ABK84841	Abk84841 DNA fragm	217	16.8	60.0	906	8	ACA41677	ACA41677 Prokaryot
c 145	17.4	62.1	6612	3	AAAC64963	Aac64963 C. elegan	218	16.8	60.0	936	11	ABD12893	Abd12893 Pseudomon
c 146	17.4	62.1	6612	6	ABK84843	Abk84843 DNA fragm	219	16.8	60.0	1067	12	ADQ63330	Adq63330 Transcrip
c 147	17.4	62.1	11207	3	AAAC64960	Aac64960 C. elegan	220	16.8	60.0	1116	10	ABZ50307	Abz50307 A. thalia
c 148	17.4	62.1	11207	6	ABK84840	Abk84840 Cogmid K1	221	16.8	60.0	1179	6	ABQ30075	Abq30075 Oligonucl
c 149	17.4	62.1	11438	6	ABK84832	Abk84832 pDM2600 C	222	16.8	60.0	1179	6	ABQ30074	Abq30074 Oligonucl
c 150	17.4	62.1	11444	6	ABK84831	Abk84831 pDM2600 C	223	16.8	60.0	1257	8	ACA21389	ACA21389 Prokaryot
c 151	17.4	62.1	17678	4	ABL19341	AbL19341 Drosophil	224	16.8	60.0	1289	13	ADT41781	Adt41781 Bacterial
c 152	17.4	62.1	18011	4	ABL20689	AbL20689 Drosophil	225	16.8	60.0	1321	3	AAC39461	Aac39461 Arabidops
c 153	17.4	62.1	27845	4	ABL20591	AbL20591 Drosophil	226	16.8	60.0	1654	13	ADR56535	Adr56535 Cotton cd
c 154	17.4	62.1	31737	10	ACF67367 ⁰³	Acf67367 Photorhab	227	16.8	60.0	1657	6	ABQ70507	Abq70507 Listeria
c 155	17.4	62.1	39726	9	ABL57448	AbL57448 Human NSD	228	16.8	60.0	1746	11	ABD01202	Abd01202 Klebsiell
c 156	17.4	62.1	48718	4	ABL20590	AbL20590 Drosophil	229	16.8	60.0	2361	8	ACA41419	ACA41419 Prokaryot
c 157	17.4	62.1	63284	4	ABL20688	AbL20688 Drosophil	230	16.8	60.0	2615	10	ABZ39121	Abz39121 N. gonorr
c 158	17.4	62.1	71962	4	ABL19340	AbL19340 Drosophil	231	16.8	60.0	2615	12	ADI29368	Adi29368 Mouse MAR
c 159	17.4	62.1	110000	10	ACF65383 ²	Continuation (3 of	232	16.8	60.0	3210	12	ADI43146	Adi43146 Plant tra
c 160	17.4	62.1	110000	10	ACF65383 ²	Continuation (4 of	233	16.8	60.0	3210	12	ADO03245	Ado03245 Corn orth
c 161	17.4	62.1	115780	13	ABD32610 ⁰³	Abd32610 Mouse can	234	16.8	60.0	3210	12	ADO62538	Ado62538 Transcrip
c 162	17.4	62.1	145068	13	ABD33090	Abd33090 Murine ca	235	16.8	60.0	3867	4	ABL28028	AbL28028 Drosophil
c 163	17.4	62.1	235070	11	ACN45174	Acn45174 Human gen	236	16.8	60.0	5965	4	ABL05674	AbL05674 Human rep
c 164	17.2	61.4	300	4	ABL27933	AbL27933 Drosophil	237	16.8	60.0	5965	4	ABA07992	AbA07992 Human ova
c 165	17.2	61.4	1050	8	ADA72690	Ada72690 Rice gene	238	16.8	60.0	10945	13	ADR32078	Adr32078 Genomic D
c 166	17.2	61.4	1428	13	ADS57489	Ads57489 Bacterial	239	16.8	60.0	10945	13	ADR67768	Adr67768 West Nile

240	16.8	60.0	10962	12	ADK13681	Adk13681 West Nile	313	16.6	59.3	10091	2	AAV69642	Aav69642 Drosophil
241	16.8	60.0	10975	12	ADN98022	Adn98022 West Nile	314	16.6	59.3	25885	10	ADC86256	Adc86256 Human GPC
242	16.8	60.0	11023	8	ABZ68481	Abz68481 Nucleotid	315	16.6	59.3	31034	4	ABL13678	Ab13678 Drosophil
243	16.8	60.0	11029	10	ABV74821	Abv74821 West Nile	316	16.6	59.3	43011	12	ADN01941	Adn01941 Staphyloc
244	16.8	60.0	11029	12	ADN98023	Adn98023 West Nile	C 317	16.6	59.3	60873	3	AAA81469	Aaa81469 N. mening
245	16.8	60.0	12790	4	AAS46237	Aas46237 DNA encod	318	16.6	59.3	110000	3	AAA81490	Aaa81490 N. mening
246	16.8	60.0	17651	4	AAS59519	Aas59519 Propionib	C 319	16.6	59.3	110000	10	ABS56454	AbS56454 02
247	16.8	60.0	17651	4	ACF64448	Acf64448 Propionib	320	16.6	59.3	110000	3	ABS56454	AbS56454 06
248	16.8	60.0	22345	4	ABL02352	Ab102352 Drosophil	321	16.6	59.3	110000	10	ABS56454	AbS56454 06
C 249	16.8	60.0	38234	11	ACN45022	Adn45022 Human gen	C 322	16.6	59.3	110000	13	ACN45172	Adn45172 Mouse gen
C 250	16.8	60.0	46593	3	AAA81456	Aaa81456 N. mening	323	16.6	59.3	134841	11	ACN45172	Adn45172 Mouse gen
C 251	16.8	60.0	49767	3	AAA81458	Aaa81458 N. mening	324	16.6	59.3	143899	6	AAA81458	Aaa81458 N. mening
C 252	16.8	60.0	95914	13	ABD33444	Abd33444 Human can	C 325	16.6	59.3	348101	12	ADQ971146	Adq971146 Human can
C 253	16.8	60.0	110000	3	AAA81489	Adn81489 5	C 326	16.6	59.3	349880	2	AAF21610	Aaf21610 Neisseria
C 254	16.8	60.0	110000	3	AAA81489	Adn81489 6	327	16.6	58.6	214	6	ABR64434	AbR64434 Human ben
C 255	16.8	60.0	110000	3	AAA81489	Adn81489 7	328	16.6	58.6	214	6	ABR64434	AbR64434 Human ben
C 256	16.8	60.0	172325	3	AAF21613	Aaf21613 Neisseria	C 329	16.4	58.6	290	3	AAA00762	Aaa00762 Gene #180
C 257	16.8	60.0	188794	12	ADQ59476	Adq59476 Human can	C 330	16.4	58.6	316	13	ADS54663	AdS54663 Bacterial
C 258	16.8	60.0	349980	3	AAF21612	Aaf21612 Neisseria	C 331	16.4	58.6	364	2	AAQ59802	Aaq59802 Human bra
C 259	16.8	60.0	349980	3	AAF21612	Aaf21612 Neisseria	332	16.4	58.6	390	5	AAH65657	Aah65657 C glutami
C 260	16.6	59.3	100	8	ACD69720	Acd69720 E. coli K	333	16.4	58.6	390	8	ACA00090	Acca00090 C. glutam
C 261	16.6	59.3	297	10	ABX82062	Abx82062 Corn ear-	334	16.4	58.6	393	4	AAH76027	Aah76027 DNA encod
C 262	16.6	59.3	360	5	AAK54283	Aak54283 Murine tr	C 335	16.4	58.6	442	10	ADF80484	Adf80484 Leukaemia
C 263	16.6	59.3	409	4	AAK54136	Aak54136 Murine tr	C 336	16.4	58.6	475	4	AAI01740	Aai01740 Human rep
C 264	16.6	59.3	444	11	ADM65372	Adm65372 NRY polym	C 337	16.4	58.6	475	4	ABL97033	Ab197033 Human tes
C 265	16.6	59.3	487	10	ADC77133	Adc77133 DNA homol	C 338	16.4	58.6	504	6	ABQ30555	Abq30555 Oligonucle
C 266	16.6	59.3	487	10	ADK59424	Adk59424 Plant DNA	C 339	16.4	58.6	504	6	ABQ30554	Abq30554 Oligonucle
C 267	16.6	59.3	504	12	ACH74791	Ach74791 Human gen	C 340	16.4	58.6	612	5	AAH67960	Aah67960 C glutami
C 268	16.6	59.3	591	8	ABZ54114	Abz54114 Aspergill	C 341	16.4	58.6	614	6	ABQ50702	Abq50702 Oligonucle
C 269	16.6	59.3	669	8	ACF72930	Acf72930 Staphyloc	342	16.4	58.6	614	6	ABQ50703	Abq50703 Oligonucle
C 270	16.6	59.3	702	2	AAV74625	Aav74625 Staphyloc	C 343	16.4	58.6	615	8	ACA02097	Acca02097 C. glutam
C 271	16.6	59.3	768	10	ADC76882	Adc76882 DNA homol	C 344	16.4	58.6	621	13	ADS57054	AdS57054 Bacterial
C 272	16.6	59.3	792	10	ADH82410	Adh82410 Enterococ	345	16.4	58.6	630	4	AAAS25520	Aaas25520 Human ova
C 273	16.6	59.3	829	10	ABX06024	Abx06024 S. pneumo	C 346	16.4	58.6	631	8	ACA37473	Acca37473 Prokaryot
C 274	16.6	59.3	831	10	ABQ06527	Abq06527 S. pneumo	C 347	16.4	58.6	657	6	ABQ31721	Abq31721 Oligonucle
C 275	16.6	59.3	851	2	AAV52494	Aav52494 Streptoco	C 348	16.4	58.6	657	6	ABQ31720	Abq31720 Oligonucle
C 276	16.6	59.3	876	2	AAQ04535	Aaq04535 Polypepti	349	16.4	58.6	682	6	ABQ65760	Abq65760 Arabidops
C 277	16.6	59.3	891	8	ACA47337	Acca47337 Prokaryot	C 350	16.4	58.6	742	11	ADL65988	AdL65988 C. glutam
C 278	16.6	59.3	909	8	ABZ51282	Abz51282 Aspergill	351	16.4	58.6	768	4	AAAS24348	Aaas24348 Human ova
C 279	16.6	59.3	932	3	ACA54942	Aca54942 Arabidops	352	16.4	58.6	778	5	AAH82937	Aah82937 Human ova
C 280	16.6	59.3	936	3	ACA35411	Aca35411 Arabidops	353	16.4	58.6	988	6	ABQ47291	Abq47291 Oligonucle
C 281	16.6	59.3	1058	10	ADC77137	Adc77137 DNA homol	C 354	16.4	58.6	988	6	ABQ47290	Abq47290 Oligonucle
C 282	16.6	59.3	1058	10	ADK59428	Adk59428 Plant DNA	C 355	16.4	58.6	1029	13	ADS55698	AdS55698 Bacterial
C 283	16.6	59.3	1058	10	ADK55693	Adk55693 Plant DNA	C 356	16.4	58.6	1037	3	AAAS2043	Aaas2043 Arabidops
C 284	16.6	59.3	1149	10	ABZ39764	Abz39764 N. gonorr	C 357	16.4	58.6	1137	13	ADS50184	AdS50184 Bacterial
C 285	16.6	59.3	1191	10	ADC77296	Adc77296 DNA homol	C 358	16.4	58.6	1359	5	AAAS88887	Aaas88887 DNA encod
C 286	16.6	59.3	1191	10	ADC77296	Adc77296 DNA homol	C 359	16.4	58.6	1361	12	ADJ74952	Adj74952 Marker ge
C 287	16.6	59.3	1200	8	ACA57183	Acca57183 Plant DNA	C 360	16.4	58.6	1361	12	ADN04871	Adn04871 Antipsori
C 288	16.6	59.3	1221	6	ABQ41561	Abq41561 Oligonucle	C 361	16.4	58.6	1361	13	ADP25040	Adp25040 PRO polyp
C 289	16.6	59.3	1221	6	ABQ41560	Abq41560 Oligonucle	362	16.4	58.6	1365	3	AAAS2043	Aaas2043 Arabidops
C 290	16.6	59.3	1223	6	ABQ44567	Abq44567 Oligonucle	C 363	16.4	58.6	1404	4	AAI58819	Aai58819 Human pol
C 291	16.6	59.3	1223	6	ABQ44566	Abq44566 Oligonucle	C 364	16.4	58.6	1404	5	ADQ99040	Adq99040 DNA encod
C 292	16.6	59.3	1275	8	ADA70826	Ada70826 Rice gene	C 365	16.4	58.6	1404	9	ADB48800	Adb48800 Novel hum
C 293	16.6	59.3	1579	4	ABL01941	Ab101941 Drosophil	366	16.4	58.6	1455	5	AAH67851	Aah67851 C glutami
C 294	16.6	59.3	1584	8	ACA23970	Acca23970 Prokaryot	367	16.4	58.6	1473	2	AAAX91565	Aaax91565 Porphorym
C 295	16.6	59.3	1704	13	ADS58889	AdS58889 Bacterial	368	16.4	58.6	1496	2	AAAX07336	Aaax07336 Arabidops
C 296	16.6	59.3	1731	4	ABL08345	Ab108345 Drosophil	C 369	16.4	58.6	1513	4	AAAS41001	Aaas41001 cDNA enco
C 297	16.6	59.3	1974	13	ADT42349	Adt42349 Bacterial	C 370	16.4	58.6	1546	4	AAF71762	Aaf71762 Corynebac
C 298	16.6	59.3	2000	12	ADJ41159	Adj41159 plant cDN	371	16.4	58.6	1578	4	AAF71761	Aaf71761 Corynebac
C 299	16.6	59.3	2558	2	AAV53514	Aav53514 DNA encod	372	16.4	58.6	1578	6	ABAS65356	Abas65356 DNA encod
C 300	16.6	59.3	2666	9	ADB84031	Adb84031 Japanese	373	16.4	58.6	1579	6	AAA89277	Aaa89277 Arabidops
C 301	16.6	59.3	2860	10	ADC37168	Adc37168 Nuclear f	374	16.4	58.6	1623	3	AAAC49050	Aaac49050 Arabidops
C 302	16.6	59.3	3636	4	AAAS51642	Aaas51642 Staphyloc	375	16.4	58.6	1626	3	AAAC37639	Aaac37639 Arabidops
C 303	16.6	59.3	3697	4	ABL01940	Ab101940 Drosophil	376	16.4	58.6	1677	9	ADB09439	Adb09439 Alloiooc
C 304	16.6	59.3	3793	4	ABL08344	Ab108344 Drosophil	377	16.4	58.6	1754	3	AAAS3743	Aaas3743 Plant tra
C 305	16.6	59.3	4437	8	ACF73516	Acf73516 Staphyloc	378	16.4	58.6	2369	6	ABK15556	Abk15556 DNA encod
C 306	16.6	59.3	4449	4	AAAS4749	Aaas4749 Staphyloc	379	16.4	58.6	2748	12	ADM57406	Adm57406 T gondii
C 307	16.6	59.3	4585	4	ABL28758	Ab128758 Drosophil	380	16.4	58.6	3010	6	AAAL48965	Aaal48965 C glutami
C 308	16.6	59.3	4594	2	AAAX13167	Aax13167 Enterococ	C 381	16.4	58.6	3040	4	AAHS4425	Aahs4425 S. epider
C 309	16.6	59.3	4594	6	ABAS98962	Abas98962 Enterococ	C 382	16.4	58.6	3050	8	ABZ10011	Abz10011 Haematopo
C 310	16.6	59.3	5148	8	ADA68320	Ada68320 Arabidops	C 383	16.4	58.6	3050	13	ACS89359	Accs89359 Oligonucle
C 311	16.6	59.3	9372	10	ADD15194	Ad15194 Human DFF	C 384	16.4	58.6	3128	11	ACN88838	Accn88838 Breast ca
C 312	16.6	59.3	9372	12	ADM33394	Adm33394 Human PRO	385	16.4	58.6	3187	5	AAAS88889	Aaas88889 DNA encod

C 386	16.4	58.6	3870	8	ABZ42676	Abz42676 Human his	C 459	16.2	57.9	730	3	AAZ80609	Aaz80609 Human col
C 387	16.4	58.6	4008	12	ADL12429	Adl12429 Human ste	C 460	16.2	57.9	885	8	ACA53118	Acas3118 Prokaryot
C 388	16.4	58.6	4057	4	AH54243	Aah54243 S. epider	C 461	16.2	57.9	984	8	ACA51543	Acas1543 Prokaryot
C 389	16.4	58.6	4154	10	ADD47133	Add47133 Human gen	C 462	16.2	57.9	989	8	ACA48835	Acas4835 Prokaryot
C 390	16.4	58.6	4242	4	ABL05330	Ab105330 Drosophill	C 463	16.2	57.9	1056	4	AAD05228	Aad05228 Human sec
C 391	16.4	58.6	4270	4	ABL08659	Ab108659 Drosophill	C 464	16.2	57.9	1089	4	AAS44619	Aas44619 Human ful
C 392	16.4	58.6	4307	13	ACN42407	Acn42407 Human dia	C 465	16.2	57.9	1091	4	AAS44791	Aas44791 Human con
C 393	16.4	58.6	4321	13	ACN42408	Acn42408 Human dia	C 466	16.2	57.9	1112	6	ABQ42887	Abq42887 Oligonuc1
C 394	16.4	58.6	4321	13	ACN42408	Acn42408 Human dia	C 467	16.2	57.9	1112	6	ABQ42886	Abq42886 Oligonuc1
C 395	16.4	58.6	4580	4	ABL12621	Ab112621 Drosophill	C 468	16.2	57.9	1194	5	ADL63507	Adl63507 Human ova
C 396	16.4	58.6	4848	6	ABQ70991	Abq70991 Listeria	C 469	16.2	57.9	1225	3	ACA54094	Acas4094 Arabidops
C 397	16.4	58.6	5401	4	ABL11443	Ab111443 Drosophill	C 470	16.2	57.9	1232	3	ACA37247	Acac37247 Arabidops
C 398	16.4	58.6	5768	10	ADES9601	Ades9601 Human gen	C 471	16.2	57.9	1232	3	ACA37247	Acac37247 Arabidops
C 399	16.4	58.6	5856	10	ACF63378	Acf63378 Human his	C 472	16.2	57.9	1299	6	ABZ14542	Abz14542 Arabidops
C 400	16.4	58.6	5994	6	ABL32879	Ab132879 Human imm	C 473	16.2	57.9	1299	6	ADN68548	Adn68548 Arabidops
C 401	16.4	58.6	6050	6	AAS46791	Aas46791 Tumour su	C 474	16.2	57.9	1299	12	ADN74748	Adn74748 Thale Gre
C 402	16.4	58.6	6050	6	ABL34128	Ab134128 Human imm	C 475	16.2	57.9	1304	8	ABQ83878	Abq83878 Human MDD
C 403	16.4	58.6	6050	6	ABL34128	Ab134128 Human imm	C 476	16.2	57.9	1308	8	AA104369	Aal04369 Human rep
C 404	16.4	58.6	6050	6	ABK33936	Abk33936 Human DNA	C 477	16.2	57.9	1454	3	AAC54201	Aac54201 Arabidops
C 405	16.4	58.6	6050	8	ADA20384	Ada20384 Prostate	C 478	16.2	57.9	1457	3	AAC53243	Aac53243 Arabidops
C 406	16.4	58.6	6050	8	ADA84191	Ada84191 Human ren	C 479	16.2	57.9	1540	10	ADP82111	Adp82111 Leukaemia
C 407	16.4	58.6	6235	10	ADE84105	Ades84105 Human lym	C 480	16.2	57.9	1643	10	ADA52947	Ada52947 Human cod
C 408	16.4	58.6	6235	6	ABL32786	Ab132786 Human imm	C 481	16.2	57.9	2000	12	ADJ40878	Adj40878 Plant CDN
C 409	16.4	58.6	6567	4	ABL08658	Ab108658 Drosophill	C 482	16.2	57.9	2004	5	AAH75921	Aah75921 Human ATP
C 410	16.4	58.6	6580	4	ABL12620	Ab112620 Drosophill	C 483	16.2	57.9	2311	5	AAH75921	Aah75921 DNA encod
C 411	16.4	58.6	7106	13	ADT05458	Adt05458 Haemophil	C 484	16.2	57.9	2715	13	ADS48830	Ades48830 Bacterial
C 412	16.4	58.6	7309	6	AAS46567	Aas46567 Tumour su	C 485	16.2	57.9	2733	10	ADE55479	Ades5479 Rat gene
C 413	16.4	58.6	7309	6	ABL33816	Ab133816 Human imm	C 486	16.2	57.9	2733	10	ADE55475	Ades5475 Rat gene
C 414	16.4	58.6	7309	13	ADBS4163	Adbs4163 Pretreat	C 487	16.2	57.9	2733	10	ADE55487	Ades5487 Rat gene
C 415	16.4	58.6	7309	13	ADBS4163	Adbs4163 Pretreat	C 488	16.2	57.9	2733	10	ADE55483	Ades5483 Rat gene
C 416	16.4	58.6	7611	4	ABL11442	Ab111442 Drosophill	C 489	16.2	57.9	3450	4	AAA91119	Aaa91119 Apaf-1XL
C 417	16.4	58.6	9474	6	ABK50462	Abk50462 Human his	C 490	16.2	57.9	3618	4	AAA91116	Aaa91116 Apaf-1L c
C 418	16.4	58.6	13606	4	AAS45458	Aas45458 Chemicall	C 491	16.2	57.9	3635	12	ADM86936	Adm86936 Human pro
C 419	16.4	58.6	13606	4	AAS45458	Aas45458 Chemicall	C 492	16.2	57.9	3710	10	ADE55485	Ades5485 Human gen
C 420	16.4	58.6	13606	6	ABL33811	Ab133811 Human imm	C 493	16.2	57.9	3710	10	ADE55481	Ades5481 Human gen
C 421	16.4	58.6	13606	6	ABK28314	Abk28314 DNA trans	C 494	16.2	57.9	3710	10	ADE55477	Ades5477 Human gen
C 422	16.4	58.6	18167	4	ABL06096	Ab106096 Drosophill	C 495	16.2	57.9	3714	4	AAA91117	Aaa91117 Apaf-1XL
C 423	16.4	58.6	84707	6	ABQ67196	Abq67196	C 496	16.2	57.9	3747	4	AAA91122	Aaa91122 Apaf-1XL
C 424	16.4	58.6	100608	13	ABD32769	Abd32769 Human can	C 497	16.2	57.9	3747	4	AAA91120	Aaa91120 Apaf-1XL
C 425	16.4	58.6	110000	6	ABQ69245	Abq69245	C 498	16.2	57.9	3747	4	AAA91118	Aaa91118 Apaf-1XL
C 426	16.4	58.6	110000	8	AAD53224	Ad53224	C 499	16.2	57.9	3747	4	AAA91125	Aaa91125 Apaf-1XL
C 427	16.4	58.6	110000	9	ABD12064	Abd12064	C 500	16.2	57.9	3747	4	AAA91124	Aaa91124 Apaf-1XL
C 428	16.4	58.6	110000	10	ADF77343	Adf77343							
C 429	16.4	58.6	110000	11	ACN43998	Acn43998							
C 430	16.4	58.6	175590	10	ADD50650	Add50650							
C 431	16.4	58.6	349980	5	AAH68525	Aah68525							
C 432	16.4	58.6	349980	5	AAH68525	Aah68525							
C 433	16.4	58.6	349980	5	AAH68533	Aah68533							
C 434	16.2	57.9	299	9	ABK54748	Abk54748 Human col							
C 435	16.2	57.9	434	9	ACH21812	Ach21812 Human adu							
C 436	16.2	57.9	457	8	ABZ54905	Abz54905 Aspergill							
C 437	16.2	57.9	492	5	ADL44430	Adl44430 Human ova							
C 438	16.2	57.9	493	3	AAA06669	Aaa06669 Human imm							
C 439	16.2	57.9	493	4	AAH93785	Aah93785 Human pro							
C 440	16.2	57.9	493	4	AAH63878	Aah63878 Human pro							
C 441	16.2	57.9	493	4	AAH02850	Aah02850 Prostate							
C 442	16.2	57.9	493	4	AAH85099	Aah85099 Human pro							
C 443	16.2	57.9	493	5	ACA59686	Acas59686 Prostate							
C 444	16.2	57.9	493	5	ABL95249	Ab195249 Human 236							
C 445	16.2	57.9	493	8	ACC95413	Acc95413 Prostate							
C 446	16.2	57.9	493	10	ADL13900	Adl13900 Human pro							
C 447	16.2	57.9	493	10	ADG36316	Adg36316 Human pro							
C 448	16.2	57.9	509	3	ACA37295	Ac37295 Arabidops							
C 449	16.2	57.9	525	6	ABV87129	Abv87129 Human col							
C 450	16.2	57.9	538	12	ACH71924	Ach71924 Human gen							
C 451	16.2	57.9	539	10	ADG38307	Adg38307 Aspergill							
C 452	16.2	57.9	559	6	ABV87210	Abv87210 Human col							
C 453	16.2	57.9	613	6	ABN64627	Abn64627 Human can							
C 454	16.2	57.9	623	6	ABV89076	Abv89076 Human col							
C 455	16.2	57.9	644	3	AAF12943	Aaf12943 Aspergill							
C 456	16.2	57.9	657	5	ADL38046	Adl38046 Human ova							
C 457	16.2	57.9	657	5	ADI72908	Adi72908 Human ova							
C 458	16.2	57.9	693	3	AAA78465	Aaa78465 Plant SDF							

ALIGNMENTS

RESULT 1

ABX15698
ID ABX15698 standard; DNA; 28 BP.

XX AC ABX15698;
XX 31-MAR-2003 (first entry)
XX Dengue virus detection PCR primer #2.

XX PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF;
XX dengue haemorrhagic fever; virus; viral detection.

XX Dengue virus.

XX US2002155435-A1.

XX 24-OCT-2002.

XX 28-FEB-2002; 2002US-00085944.

XX 01-MAR-2001; 2001US-0272535P.

XX (WANG/) WANG W.

XX Wang W;

XX WPI; 2003-182625/18.

XX New dengue virus-specific primers, useful for reverse transcriptase-
PT polymerase chain reaction assays, particularly for detecting or
PT quantitating dengue virus in a sample.

XX Claim 28; Page 1; 6pp; English.

XX This invention relates to novel Dengue virus reverse transcriptase (RT)
CC PCR primers which may be used to detect Dengue virus in a sample. Dengue
CC virus is a member of the flavivirus family and causes diseases including
CC dengue fever (DF) and dengue haemorrhagic fever. The invention also
CC comprises a method for detecting and quantitating dengue virus. The
CC dengue virus-specific primers of the invention are useful in reverse
CC transcriptase-polymerase chain reaction assays, particularly for
CC detecting or quantitating dengue virus in a sample. The present sequence
CC represents a dengue virus specific RT-PCR primer used in the method of
CC the invention

XX SQ Sequence 28 BP; 11 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||

RESULT 2
ADR47007
ID ADR47007 standard; DNA; 2328 BP.

XX AC ADR47007;

XX 18-NOV-2004 (first entry)

XX Dengue virus DNA for vaccine.

DE ds; gene; cytostatic; virucide; dengue virus; recombinant replicon;
KW deletion; preM protein; C protein; NS1 protein signal; vaccine;
KW cervical cancer; viral disease; antigen; dendritic cell; immune response;
KW human papillomavirus.

XX Dengue virus.

OS WO2004072274-A1.

XX 26-AUG-2004.

XX 30-JAN-2004; 2004WO-CN000088.

XX 30-JAN-2003; 2003CN-00115272.

XX 30-JAN-2003; 2003CN-00115273.

XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA (TENG-) TENGGEN BIOMEDICAL CO.
PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

XX Pang X;

XX WPI; 2004-625870/60.

XX Virus-like particle vaccines containing dengue virus recombinant replicon
PT as core for carrier, applicable in preventives or/and remedies for tumors
PT like cervical cancer and viral diseases.

XX Claim 3; SEQ ID NO 4; 38pp; Chinese.

XX A dengue virus recombinant replicon has a deletion of the complete coding
CC sequence for preM protein of dengue virus and also includes elements of

CC e.g. the non-coding region in the whole of the 5'-end, the coding region
CC of the front 20 amino acids in the C protein, and the coding region of
CC NS1 protein signal; coding regions of all non-structural proteins. The
CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to a Dengue virus DNA sequence used in
CC the recombinant replicon of the invention.

XX SQ Sequence 2328 BP; 775 A; 468 C; 585 G; 500 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 13; Length 2328;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67
|||||

RESULT 3
ABX13740
ID ABX13740 standard; DNA; 2357 BP.

XX AC ABX13740;

XX 28-FEB-2003 (first entry)

XX Dengue virus type 2 structural gene genome segment.

DE Pharmaceutical; ds; immune response; immunogenic; envelope; membrane;
KW preM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen;
KW mosquito; Aedes aegyptii; acute undifferentiated fever;
KW dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS;
KW immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
KW structural gene; virucide.

XX Dengue virus.

OS US6455509-B1.

XX 24-SEP-2002.

XX 04-JUN-1997; 97US-00869423.

XX 04-JUN-1996; 96US-0017839P.

XX (USNA) US SEC OF NAVY.

XX Kocheil TJ, Porter KR, Raviprakash K, Hoffman SL, Hayes CG;
XX WPI; 2003-066244/06.

XX New pharmaceutical compositions containing dengue nucleic acids, useful
PT as a vaccine, particularly for inducing a protective immune response in
PT mammalian subjects against the dengue virus infection.

XX Disclosure; Col 17-20; 26pp; English.

XX The invention discloses a pharmaceutical composition capable of inducing
CC an immune response in a mammalian subject, comprising an immunogenic
CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
CC which includes the envelope and membrane (preM) genes of a dengue type 1,
CC 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of
CC the family Flaviviridae and is a positive strand RNA virus encoding ten

CC proteins. These genes are translated as a polyprotein which is cleaved by
CC host and viral proteinases. The virus envelope protein is a major antigen
CC which can be targeted by neutralising antibodies. The membrane protein
CC also appears on the virion surface and is required for proper processing
CC of the envelope protein. Dengue viruses are transmitted primarily by the
CC mosquito, *Aedes aegypti*, and can lead to human illnesses ranging from
CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and
CC dengue shock syndrome (DSS). Secondary infections, with a different
CC serotype, may lead to an immune enhancement phenomenon. The compositions
CC of the invention are DNA vaccines which are injected into the animal as a
CC technique of gene therapy. The composition is useful as a vaccine,
CC particularly for inducing a protective immune response in mammalian
CC subjects against the dengue virus infection. The sequence presented is
CC the dengue virus type 2 (Den 2) structural gene genome segment
XX
SQ Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 8; Length 2357;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
Db 60 AATATGCTGAACCGGAGAGAAACCGCG 87

RESULT 4
ADG93319
ID ADG93319 standard; DNA; 2423 BP.
XX
AC ADG93319;
XX
DT 11-MAR-2004 (first entry)
XX
DE DEN1 (Puerto Rico/94) ME chimeric region DNA SeqID52.
XX
KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetraivalent vaccine;
KW dengue virus; delta30; attenuating mutation; humoral response;
KW cellular response; non-structural protein; structural protein;
KW dengue virus serotype; gene; ds; plasmid P2.
XX
OS Dengue virus type 1.
XX
PN WO2003092592-A2.
XX
PD 13-NOV-2003.
XX
PF 25-APR-2003; 2003WO-US013279.
XX
PR 03-MAY-2002; 2002US-0377860P.
PR 23-DEC-2002; 2002US-0436500P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
PI Hanley K;
XX
DR WPI; 2004-022612/02.
DR P-PSDB; ADG93320.
XX
PT New tetraivalent vaccine containing a common nucleotide deletion in the 3'
PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT of disease in humans caused by dengue virus, or for inducing immune
PT response.
XX
PS Disclosure; SEQ ID NO 52; 181pp; English.
XX
CC This invention relates to a novel immunogenic composition being
CC tetraivalent and containing a common nucleotide deletion in the 3'
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetraivalent vaccine is

CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetraivalent vaccine, the new tetraivalent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC) structural proteins present in each dengue virus serotype. The present
CC sequence is that of the DEN1 ME chimeric region DNA which is related to
CC the invention.
XX

SQ Sequence 2423 BP; 747 A; 513 C; 636 G; 527 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 2423;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
Db 138 AATATGCTGAACCGGAGAGAAACCGCG 165

RESULT 5
AAT47666
ID AAT47666 standard; cDNA; 3381 BP.
XX
AC AAT47666;
XX

DT 17-OCT-2003 (revised)
DT 19-MAY-1997 (first entry)

DE Dengue virus serotype 2 PR159/S1 mutant sequence.

DE DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.

OS Dengue virus; serotype 2.

Key Location/Qualifiers
mutation 1216..1218
/*tag= a
/note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
is GAA (Glu) in wild-type PR159"
mutation 1258..1260
/*tag= b
/note= "codon GTT (Val) at position 1258-1260 of PR159/S1
is GTG (Val) in wild-type PR159"
mutation 1762..1764
/*tag= c
/note= "codon GTT (Val) at position 1762-1764 of PR159/S1
is ATT (Ile) in wild-type PR159"
mutation 1927..1929
/*tag= d
/note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
is AGT (Ser) in wild-type PR159"

WO9637221-A1.

28-NOV-1996.

24-MAY-1996; 96WO-US007627.

24-MAY-1995; 95US-00448734.

07-JUN-1995; 95US-00488807.

10-JUL-1995; 95US-00500469.

(HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.

Ivy JM, Nakano E, Clements D;

WPI; 1997-020938/02.

P-PSDB; AAW09409.

Sub:unit vaccine against flavivirus infection - contg. recombinant

PT envelope protein in secretatable form, used for immunising against
 PT flavivirus infection.

XX Example 1; Fig 3A-D; 12lpp; English.

XX A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
 CC shows 4 differences from the wild-type DEN-2 PR159. This results in a
 CC conservative mutation in domain B of S1 that may be involved in the
 CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA
 CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of
 CC the virus. The clone can be used to express recombinant secreted
 CC polypeptides, comprising portions of the envelope protein (esp. domain B,
 CC Gly296-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and
 CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral
 CC infection. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 3381;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28

DB 40 AATATGCTGAACCGCGAGAGAAACCGCG 67

RESULT 6

AAAX25114

ID AAX25114 standard; cDNA; 3381 BP.

XX AAX25114;

AC AAX25114;

DT 17-OCT-2003 (revised)

DT 05-JUL-1999 (first entry)

XX Dengue virus serotype 2 PR159/S1 viral capsid, prM, E, NS1 cDNA.

XX Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.

XX Dengue virus; serotype 2.

XX WO9906068-A2.

XX 11-FEB-1999.

XX 27-JUL-1998; 98WO-US015447.

XX 31-JUL-1997; 97US-00904227.

XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.

XX Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KB;

XX WPI; 1999-153454/13.

XX P-PSDB; AAY05522.

XX Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
 PT 80% E protein, useful for protecting against flavivirus, especially dengue
 PT virus infections.

XX Example 1; Fig 3A-D; 60pp; English.

XX This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins
 CC (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
 CC strain served as the source for DEN-2 genes used in the invention. A
 CC vaccine for protecting against flavivirus infection comprises a dimeric
 CC 80% E protein that has been secreted as a recombinant protein from a
 CC eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.
 CC The dimeric truncated E is formed: (1) by directly linking 2 tandem
 CC copies of 80% E via a flexible tether; (2) via the formation of a leucine
 CC zipper domain through the homodimeric association of 2 leucine zipper
 CC helices each fused to the C-terminus of an 80% E molecule; or (3) via the

CC formation of a non-covalently associated four-helix bundle domain formed
 CC upon association of two helix-turn-helix moieties attached to the C-
 CC terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
 CC efficiently secreted by recombinant cells, are easier to purify than
 CC intracellular proteins, and generate a high titer neutralising antibody
 CC response. The method is generally applicable to flaviviruses, in
 CC particular dengue viruses such as DEN-2, where 80% E comprises amino
 CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
 CC infection. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 3381;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28

DB 40 AATATGCTGAACCGCGAGAGAAACCGCG 67

RESULT 7

ADL98085

ID ADL98085 standard; DNA; 3381 BP.

XX ADL98085;

AC ADL98085;

DT 18-NOV-2004 (first entry)

DT Dengue virus, DEN-2, partial genome.

DE Dengue virus, DEN-2, partial genome.

XX Dengue virus; DEN-2; ss; Envelope protein; 80% E; membrane protein;

XX capsid protein; NS1 protein; Dengue haemorrhagic fever; DHF;

XX Dengue shock syndrome; DSS; flavivirus; vaccine.

XX Dengue virus type 2; strain PR159/S1.

XX Key Location/Qualifiers

FT CDS 1..3381

FT /*tag= a

FT /product= "DEN-2 Capsid-membrane-envelope-NS1 proteins"

FT /partial

FT /note= "No stop codon shown"

XX US2003175304-A1.

XX 18-SEP-2003.

XX 20-SEP-2002; 2002US-00247960.

XX 31-JUL-1997; 97US-00904227.

XX 18-AUG-1999; 99US-00376463.

XX (PETE/) PETERS I D.

XX (COLL/) COLLIER B G.

XX (MCDO/) MCDONELL M.

XX (IVYJ/) IVY J M.

XX (HARA/) HARADA K.

XX Peters ID, Collier BG, McDonnell M, Ivy JM, Harada K;

XX WPI; 2003-898503/82.

XX P-PSDB; ADL98086.

XX Vaccine useful for protection against dengue virus infection, comprises a

XX dimeric 80% envelope, which has been secreted as a recombinantly produced

XX protein from Drosophila Schneider cells.

XX Example 1; Fig 3; 3lpp; English.

XX The invention relates to a vaccine for protection against flavivirus

XX infection comprising a dimeric 80% envelope (E), which has been secreted

XX as a recombinantly produced protein from Drosophila Schneider cells and

CC which represents the N-terminal 80% portion of the protein from residue 1
 CC -395. Also included are a method for protecting a subject against a
 CC Flavivirus, an immunogenic polypeptide comprising a dimeric 80% E, an
 CC immunogenic composition for protection against Flavivirus infection
 CC comprising the immunogenic polypeptide and a carrier, an immunodiagnostic
 CC for detecting Flavivirus comprising the immunogenic polypeptide, a vector
 CC host recombinant DNA expression system, a DNA sequence encoding the
 CC immunogenic polypeptide and an immunodiagnostic kit for detecting
 CC Flavivirus in a test subject. The dimeric 80% E products are envelope
 CC proteins of serotypes comprising DEN-1, DEN-2, DEN-3 or DEN-4. The
 CC Flavivirus is a dengue virus. The 80% E protein is produced as a dimer by
 CC incorporating 2 different kinds of leucine zipper peptides or
 CC incorporating a helix-turn-helix peptide, to encourage dimerization. The
 CC vaccine is useful for protection against dengue virus infection (e.g.
 CC Dengue haemorrhagic fever, DHF, and Dengue shock syndrome, DSS). The
 CC present sequence is the partial genomic sequence of the DEN-2 strain
 CC PR159/S1 virus, encoding the capsid, membrane, envelope and NS1 proteins.
 XX
 SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 11; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.013; Length 3381;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67
 |||||

RESULT 8

ADQ28715
 ID ADQ28715 standard; DNA; 3381 BP.

AC ADQ28715;

XX 26-AUG-2004 (first entry)

XX Dengue virus viral capsid, prM, E and NS1 genes.

XX virucide; vaccine; Flavivirus; dimeric 80%E; Drosophila Schneider cell;
 KW immunogenic composition; multivalent immunodiagnostic; dengue virus;
 KW viral capsid; prM gene; E gene; NS1 gene; ds.

XX Dengue virus.

XX Key Location/Qualifiers
 FT CDS 1..3381
 FT /*tag= a
 FT /product= "Dengue virus viral capsid, prM, E and NS1
 FT polypeptide"

XX US6749857-B1.

XX 15-JUN-2004.

XX 18-AUG-1999; 99US-00376463.

XX 31-JUL-1997; 97US-00904227.

XX (HAWAII) HAWAII BIOTECHNOLOGY GROUP INC.

XX Peters ID, Coller BG, McDonnell M, Ivy JM, Harada K;

XX WPI; 2004-438725/41.

DR P-PSDB; ADQ28716.

XX New vaccines for preventing or diagnosing infections caused by dengue
 PT virus comprises a therapeutic amount of a dimeric 80%E protein secreted
 PT from Drosophila Schneider cells.

XX Example 1; SEQ ID NO 2; 47pp; English.

XX The invention describes a vaccine that generates a protective,

CC neutralising antibody response to a Flavivirus in a murine host. The
 CC vaccine comprises a therapeutic amount of a dimeric 80%E, the dimeric
 CC 80%E having been secreted as a recombinantly produced protein from
 CC Drosophila Schneider cells, and where 80%E represents the N-terminal 80%
 CC portion of the protein from residues 1-395. Also described are: an
 CC immunogenic polypeptide comprising the dimeric 80%E cited above; an
 CC immunogenic composition that generates a protective, neutralising
 CC antibody response to a Flavivirus in a murine host, comprising the above
 CC immunogenic polypeptide and a physiological carrier; a multivalent
 CC immunodiagnostic for the detection of Flavivirus, comprising at least 2
 CC of the above immunogenic polypeptides of at least 2 flavivirus serotypes;
 CC and an immunodiagnostic kit for the detection of Flavivirus in a test
 CC subject, comprising the above immunogenic or multivalent immunodiagnostic
 CC polypeptide, a suitable support phase coated with dimeric 80%E, and
 CC labeled antibodies immunoreactive to antibodies from the test subject.
 CC The composition is useful for preventing or diagnosing infections caused
 CC by dengue virus. This sequence encodes Dengue virus gene viral capsid,
 CC prM, E and NS1 genes for Dengue virus strain PR159/S1 used as the source
 CC of DEN-2 genes for the invention.
 XX

SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67
 |||||

RESULT 9

AD53912

ID AAD53912 standard; DNA; 10616 BP.

XX AAD53912;

XX 28-MAY-2003 (first entry)

XX Dengue virus type 2 strain rDEN2/4delta30 DNA.

XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.

XX Dengue virus.

XX Key Location/Qualifiers
 FT CDS 97..10263
 FT /*tag= a
 FT /product= "DEN4 strain rDEN2/4delta30 protein"
 FT mat_peptide 97..438
 FT /*tag= c
 FT /product= "Anchored capsid protein"
 FT mat_peptide 97..396
 FT /*tag= b
 FT /product= "Virion capsid protein"
 FT mat_peptide 439..936
 FT /*tag= d
 FT /product= "Membrane precursor protein"
 FT mat_peptide 712..936
 FT /*tag= e
 FT /product= "Membrane protein"
 FT mat_peptide 937..2421
 FT /*tag= f
 FT /product= "Envelope protein"
 FT mat_peptide 2422..3477
 FT /*tag= g
 FT /product= "NS1 protein"
 FT mat_peptide 3478..4131
 FT /*tag= h
 FT /product= "NS2A protein"
 FT mat_peptide 4132..4521
 FT /*tag= i
 FT /product= "NS2B protein"

```

FT mat_peptide 4522..6375
FT /*tag= j
FT /product= "NS3 protein"
FT mat_peptide 6376..6756
FT /*tag= k
FT /product= "NS4A protein"
FT mat_peptide 6757..6825
FT /*tag= l
FT /product= "2K protein"
FT mat_peptide 6826..7560
FT /*tag= m
FT /product= "NS4B protein"
FT mat_peptide 7561..10260
FT /*tag= n
FT /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35314.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 135-138; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX phenotype in which the viral genome is modified by introduction of a
XX mutation, singly or in combination, taken from mutations from recombinant
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX dengue type 4 virus. The methods and compositions of the invention are
XX useful for fine tuning the attenuation and growth characteristics of
XX dengue virus vaccines for the prevention and/or treatment of dengue virus
XX infection. The present sequence is Dengue virus type 4 strain
XX rDEN2/4delta30 DNA
XX
XX Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 10; Length 10616;
XX Best Local Similarity 100.0%; Pred. No. 0.015;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||||||||||||||||||||||||
XX 136 AATATGCTGAACCGGAGAGAAACCGCG 163
XX
XX RESULT 10
XX AAD14612
XX ID AAD14612 standard; cDNA; 10648 BP.
XX
XX AC AAD14612;
XX
XX 11-SEP-2003 (revised)
XX 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-4 1036 CDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX mat_peptide 4522..6375
XX /*tag= j
XX /product= "NS3 protein"
XX mat_peptide 6376..6756
XX /*tag= k
XX /product= "NS4A protein"
XX mat_peptide 6757..6825
XX /*tag= l
XX /product= "2K protein"
XX mat_peptide 6826..7560
XX /*tag= m
XX /product= "NS4B protein"
XX mat_peptide 7561..10260
XX /*tag= n
XX /product= "NS5 protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07991.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 3; Page 373-389; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present CDNA
XX sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 4; Length 10648;
XX Best Local Similarity 100.0%; Pred. No. 0.015;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||||||||||||||||||||||||
XX 138 AATATGCTGAACCGGAGAGAAACCGCG 165
XX
XX RESULT 11
XX AAD14613
XX ID AAD14613 standard; cDNA; 10648 BP.
XX
XX AC AAD14613;
XX
XX 01-NOV-2001 (first entry)
XX
XX Attenuated, vaccine-strain DEN-4 PDK-48 variant CDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX ss.

```

XX Dengue virus; type IV.
OS Synthetic.
XX

XX Key Location/Qualifiers
FT CDS 102..10265
FT /*tag= a
FT /product= "DEN-4 PDK-48 protein variant"
FT replace(1211, T)
FT /*tag= b
FT mutation replace(1971, G)
FT /*tag= c
FT mutation replace(3182, G)
FT /*tag= d
FT mutation replace(6660, C)
FT /*tag= e
FT mutation replace(6957, A)
FT /*tag= f
FT mutation replace(7162, T)
FT /*tag= g
FT mutation replace(7546, C)
FT /*tag= h
FT mutation replace(7623, G)
FT /*tag= i

XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07992.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 4; Page 397-413; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region. DEN-4 virus passaged in primary dog kidney (PDK) cells
XX 48 times is designated as DEN-4 PDK-48 virus
XX

SQ Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;
Query Match 100.08; Score 28; DB 4; Length 10648;
Best Local Similarity 100.08; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGC 28
Db 138 AATATGCTGAACGCGAGAGAAACCGC 165

RESULT 12
AAD53911
ID AAD53911 standard; DNA; 10649 BP.
XX
XX AAD53911;
XX 28-MAY-2003 (first entry)
XX Recombinant dengue virus type 4 strain rDEN4 DNA.
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; da.
XX Dengue virus.
XX
XX Key Location/Qualifiers
FT CDS 102..10649
FT /*tag= a "DEN4 strain rDEN4 protein"
FT /product= "Anchored capsid protein"
FT /*tag= c
FT mat_peptide 102..440
FT /product= "Anchored capsid protein"
FT /*tag= b
FT mat_peptide 102..398
FT /product= "Virion capsid protein"
FT /*tag= d
FT mat_peptide 441..938
FT /product= "Membrane precursor protein"
FT /*tag= e
FT mat_peptide 714..938
FT /product= "Membrane protein"
FT /*tag= f
FT mat_peptide 939..2423
FT /product= "Envelope protein"
FT /*tag= g
FT mat_peptide 2424..3479
FT /product= "NS1 protein"
FT /*tag= h
FT mat_peptide 3480..4133
FT /product= "NS2A protein"
FT /*tag= i
FT mat_peptide 4134..4523
FT /product= "NS2B protein"
FT /*tag= j
FT mat_peptide 4524..6377
FT /product= "NS3 protein"
FT /*tag= k
FT mat_peptide 6378..6758
FT /product= "NS4A protein"
FT /*tag= m
FT mat_peptide 6638..7562
FT /product= "NS4B protein"
FT /*tag= n
FT mat_peptide 6759..6827
FT /product= "2K protein"
FT /*tag= n
FT mat_peptide 7563..10262
FT /product= "NS5 protein"
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX

```

XX PI Whitehead SS, Murphy BR, Hanley KA;
XX DR WPI; 2003-120809/11.
XX DR P-PSDB; AAE35313.
XX PT New mutated flavivirus, useful for fine tuning the attenuation and growth
XX PT characteristics of dengue virus vaccines for the prevention and/or
XX PT treatment of dengue virus infection.
XX PT Disclosure; Page 131-132; 246pp; English.
XX PS
XX CC The present invention relates to novel mutated flaviviruses comprising a
XX CC phenotype in which the viral genome is modified by introduction of a
XX CC mutation, singly or in combination, taken from mutations from recombinant
XX CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX CC mutations of dengue type 4 virus (DENV4) or mutations known to attenuate
XX CC dengue type 4 virus. The methods and compositions of the invention are
XX CC useful for fine tuning the attenuation and growth characteristics of
XX CC dengue virus vaccines for the prevention and/or treatment of dengue virus
XX CC infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
XX CC
XX SQ Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 10; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
RESULT 13
AAD53910
ID AAD53910 standard; DNA; 10649 BP.
XX AC AAD53910;
XX DT 28-MAY-2003 (first entry)
XX DE Dengue virus type 4 strain 2A DNA.
XX KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX OS Dengue virus.
XX PH
XX FT Location/Qualifiers
XX FT CDS 102..10649
XX FT /*tag= a
XX FT /product= "DEN4 strain 2A protein"
XX FT mat_peptide 102..440
XX FT /*tag= c
XX FT /product= "Anchored capsid protein"
XX FT mat_peptide 102..398
XX FT /*tag= b
XX FT /product= "Virion capsid protein"
XX FT mat_peptide 441..938
XX FT /*tag= d
XX FT /product= "Membrane precursor protein"
XX FT mat_peptide 714..938
XX FT /*tag= e
XX FT /product= "Membrane protein"
XX FT mat_peptide 939..2423
XX FT /*tag= f
XX FT /product= "Envelope protein"
XX FT mat_peptide 2424..3479
XX FT /*tag= g
XX FT /product= "NS1 protein"
XX FT mat_peptide 3480..4133
XX FT /*tag= h
XX FT /product= "NS2A protein"
XX FT mat_peptide 4134..4523

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```

FT /*tag= i
FT /product= "NS2B protein"
FT mat_peptide 4524..6377
FT /*tag= j
FT /product= "NS3 protein"
FT mat_peptide 6378..6758
FT /*tag= k
FT /product= "NS4A protein"
FT mat_peptide 6759..6827
FT /*tag= l
FT /product= "2K protein"
FT mat_peptide 6828..7562
FT /*tag= m
FT /product= "NS4B protein"
FT mat_peptide 7563..10262
FT /*tag= n
FT /product= "NS5 protein"
XX WO200295075-A1.
XX PD 28-NOV-2002.
XX XX
XX 22-MAY-2002; 2002WO-US016308.
XX PR 22-MAY-2001; 2001US-0293049P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA (BLAN/) BLANEY J E.
XX PI Whitehead SS, Murphy BR, Hanley KA;
XX DR WPI; 2003-120809/11.
XX DR P-PSDB; AAE35312.
XX PT New mutated flavivirus, useful for fine tuning the attenuation and growth
XX PT characteristics of dengue virus vaccines for the prevention and/or
XX PT treatment of dengue virus infection.
XX PS Disclosure; Page 123-126; 246pp; English.
XX CC The present invention relates to novel mutated flaviviruses comprising a
XX CC phenotype in which the viral genome is modified by introduction of a
XX CC mutation, singly or in combination, taken from mutations from recombinant
XX CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX CC mutations of dengue type 4 virus (DENV4) or mutations known to attenuate
XX CC dengue type 4 virus. The methods and compositions of the invention are
XX CC useful for fine tuning the attenuation and growth characteristics of
XX CC dengue virus vaccines for the prevention and/or treatment of dengue virus
XX CC infection. The present sequence is Dengue virus type 4 strain 2A DNA
XX CC
XX SQ Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 10; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
RESULT 14
AAD14605
ID AAD14605 standard; cDNA; 10717 BP.
XX AC AAD14605;
XX DT 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX DE Dengue virus (DENV)-2/3-VP1 chimeric cDNA.
XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;

```

KW immunogenic; viral disease; pharmaceutical; chimeric; ss.

XX Dengue virus; type II.

OS Dengue virus; type III.

OS Chimeric.

XX Key Location/Qualifiers

FT CDS 97..10266

FT /*tag= a

FT /product= "DEN-2/3-vp1 fusion protein"

XX WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07984.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
FT vaccinating against a range of dengue viruses.

XX Example 2; Page 203-219; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present CDNA
CC sequence encodes dengue virus (DEN)-2/3-vp1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 POK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC premenbrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 28; DB 4; Length 10717;

XX Best Local Similarity 100.0%; Pred. No. 0.015;

XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAACCGCG 28

DB 136 AATATGCTGAACCGGAGAGAACCGCG 163

XX RESULT 15

XX AAQ12787

XX ID AAQ12787 standard; RNA; 10723 BP.

XX AC AAQ12787;

XX 25-MAR-2003 (revised)

XX 21-NOV-1991 (first entry)

XX Dengue 2 virus genome.

XX dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.

XX

OS Dengue virus.

XX Key

FT CDS

FT 97..10272

FT /*tag= a

FT mat_peptide

FT 712..936

FT /*tag= b

FT /product= "M protein"

FT mat_peptide

FT 937..2421

FT /*tag= c

FT /product= "E protein"

FT mat_peptide

FT 2422..3477

FT /*tag= d

FT /product= "NS1"

FT mat_peptide

FT 3478..4131

FT /*tag= e

FT /product= "NS2A"

FT mat_peptide

FT 4132..4518

FT /*tag= f

FT /product= "NS2B"

FT mat_peptide

FT 4519..6375

FT /*tag= g

FT /product= "NS3"

FT mat_peptide

FT 6376..6825

FT /*tag= h

FT /product= "NS4a"

FT mat_peptide

FT 6826..7569

FT /*tag= i

FT /product= "NS4B"

FT mat_peptide

FT 7570..10269

FT /*tag= j

FT /product= "NS5"

XX

XX FR2654113-A.

XX 10-MAY-1991.

XX 09-NOV-1989; 89PR-00914724.

XX 09-NOV-1989; 89PR-00014724.

XX (INSP) INST PASTEUR.

XX Vincent D;

XX WPI; 1991-225002/31.

XX P-PSDB; AAR13166.

XX Detection and identification of Flaviviridae in biological sample - by

XX amplifying consensus sequence then hybridisation opt. followed by typing,

XX e.g. sequencing amplified prod.

XX Disclosure; Fig 3; 24pp; French.

XX The dengue 2 virus is an example of a member of the Flaviviridae which

XX can be identified using the probe pair of the invention. A species-

XX specific sequence can be amplified using the claimed oligonucleotides as

XX primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses

XX which can be identified include Japanese encephalitis virus and yellow

XX fever virus. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;

XX Query Match 100.0%; Score 28; DB 2; Length 10723;

XX Best Local Similarity 89.3%; Pred. No. 0.015;

XX Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAACCGCG 28

DB 136 ANUAGCUGAAGCGGAGAGAACCGCG 163

XX RESULT 16

AAT49303
 ID AAT49303 standard; cDNA; 10723 BP.
 XX
 AC AAT49303;
 XX

XX 27-AUG-2003 (revised)
 DT 11-SEP-1997 (first entry)
 XX

DE cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
 XX

XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 KW DHF; DSS; SS.
 XX

OS Dengue virus type 2 (strain 16681).
 XX

XX Key Location/Qualifiers
 FH 97..10272
 FT CDS
 FT /*tag= a
 FT /product= "DEN-2 polyprotein
 FT /transl_except(pos:9208..9210, aa:Xaa)"
 FT /note= "Xaa = unknown amino acid"
 XX

PN W09640933-A1.
 XX

XX 19-DEC-1996.
 XX

XX 06-JUN-1996; 96WO-US009209.
 XX

XX 07-JUN-1995; 95US-00483292.
 XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX

XX (UYMA-) UNIV MAHIDOL AT SALAYA.
 XX

XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
 PI Kinney R, Trent DW;
 XX

XX WPI; 1997-052330/05.
 DR P-PSDB; AAW06590.
 XX

XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
 PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
 PT quadravalent vaccine for protecting against Dengue virus infection.
 XX

XX Claim 23; Page 107-121; 261pp; English.
 PS

XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
 CC The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3,
 CC NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
 CC -53, may be used in the production of a quadravalent vaccine which
 CC provides immunity against all four serotypes of dengue virus. The vaccine
 CC also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
 CC a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
 CC protect against infection by all four serotypes of dengue virus, DEN-1,
 CC DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
 CC haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
 CC to produce the recombinant protein products of the DNA constructs which
 CC are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
 XX

XX Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;
 SQ

Query Match 100.0%; Score 28; DB 2; Length 10723;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
 |||||
 Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 17

AAT49304
 ID AAT49304 standard; cDNA; 10723 BP.
 XX

AC AAT49304;
 XX

XX 27-AUG-2003 (revised)
 DT 12-SEP-1997 (first entry)
 XX

DE cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
 XX

XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 KW DHF; DSS; SS.
 XX

OS Dengue virus type 2 (strain 16681).
 XX

XX Key Location/Qualifiers
 FH 57
 FT mutation
 FT /*tag= b
 FT /note= "C>T mutation"
 FT 97..10272
 FT CDS
 FT /*tag= a
 FT /product= "DEN-2 attenuated polyprotein
 FT /transl_except(pos:643..645, aa:Xaa)
 FT /transl_except(pos:1135..1137, aa:Xaa)
 FT /transl_except(pos:1393..1395, aa:Xaa)
 FT /transl_except(pos:2809..2811, aa:Xaa)
 FT /transl_except(pos:3040..3042, aa:Xaa)
 FT /transl_except(pos:9208..9210, aa:Xaa)
 FT /note= "Xaa = unknown amino acid"
 FT 524
 FT mutation
 FT /*tag= c
 FT /note= "A>T mutation, causes Asp to Val substitution"
 FT 2055
 FT mutation
 FT /*tag= d
 FT /note= "C>T mutation"
 FT 2579
 FT mutation
 FT /*tag= e
 FT /note= "G>A mutation, causes Gly to Asp substitution"
 FT 4018
 FT mutation
 FT /*tag= f
 FT /note= "C>T mutation, causes Leu to Phe substitution"
 FT 5547
 FT mutation
 FT /*tag= g
 FT /note= "C>T mutation"
 FT 6599
 FT mutation
 FT /*tag= h
 FT /note= "G>C mutation, causes Gly to Ala substitution"
 FT 8571
 FT mutation
 FT /*tag= i
 FT /note= "C>T mutation"
 XX

W09640933-A1.
 XX

XX 19-DEC-1996.
 XX

XX 06-JUN-1996; 96WO-US009209.
 XX

XX 07-JUN-1995; 95US-00483292.
 XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX (UYMA-) UNIV MAHIDOL AT SALAYA.
 XX

XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
 PI Kinney R, Trent DW;
 XX

XX WPI; 1997-052330/05.
 DR P-PSDB; AAW06591.
 XX

XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -

PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 27; Page 122-136; 261pp; English.
XX
XX This sequence encodes the polyprotein from an attenuated derivative of
CC Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
CC polyprotein comprises the capsid, pM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
CC NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
CC production of a quadravalent vaccine which provides immunity against all
CC four serotypes of dengue virus. The vaccine also comprises a chimeric DEN
CC -2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
CC The new quadravalent vaccines are used to protect against infection by
CC all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
CC can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
CC syndrome (DHF/DSS). Host cells are used to produce the recombinant
CC protein products of the DNA constructs which are used in the vaccines.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;

Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACGCGAGAGAAACCGCG 163

RESULT 18
AAD14614
ID AAD14614 standard; cDNA; 10723 BP.
XX
XX AAD14614;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VP1 chimeric cDNA.
DE
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
OS
OS Dengue virus; type II.
OS Chimeric.

Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2/1-VP1 fusion protein"

XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07993.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 5; Page 422-438; 470pp; English.

CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC premembrane/membrane protein (pM) and an envelope protein (E) from wild-
CC type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACGCGAGAGAAACCGCG 163

RESULT 19
AAD14607
ID AAD14607 standard; cDNA; 10723 BP.
XX
XX AAD14607;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-2 16681 cDNA.
XX
XX Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX Dengue virus; type II.

Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 16681 protein"

XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07986.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 3; Page 252-268; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-

CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
 CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
 CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
 CC contains 5' non-coding region followed by a capsid protein (C) encoding
 CC region, premembrane/membrane protein (prM) encoding region, an envelope
 CC protein (E) encoding region, followed by the region encoding non-
 CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
 CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
 |||||
 DB 136 AATATGCTGAACCGCGAGAGAAACCGCG 163

RESULT 20

AAD14606
 ID AAD14606 standard; cDNA; 10723 BP.

AC AAD14606;

DT 11-SEP-2003 (revised)

DT 01-NOV-2001 (first entry)

DE Dengue virus (DEN)-2/4-VPI chimeric cDNA.

KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.

OS Dengue virus; type II.

OS Dengue virus; type IV.

OS Chimeric.

FH Key Location/Qualifiers

FT CDS 97..10272

FT /*tag= a
 FT /product= "DEN-2/4-VPI fusion protein"

FT WO200160847-A2.

PN 23-AUG-2001.

PF 16-FEB-2001; 2001WO-US005142.

PR 16-FEB-2000; 2000US-0182829P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX WPI; 2001-497162/54.

XX P-PSDB; AAE07985.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
 XX vaccinating against a range of dengue viruses.

XX Example 3; Page 227-243; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras

CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes dengue virus (DEN)-2/4-VPI fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS3)-250 and the
 CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;

Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
 |||||
 DB 136 AATATGCTGAACCGCGAGAGAAACCGCG 163

RESULT 21

AAD14608
 ID AAD14608 standard; cDNA; 10723 BP.

AC AAD14608;

DT 01-NOV-2001 (first entry)

DE Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.

KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; mutein;
 KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.

OS Dengue virus; type II.

OS Synthetic.

FH Key Location/Qualifiers

FT mutation replace(57, C)

FT /*tag= b

FT CDS 97..10272

FT /*tag= a
 FT /product= "DEN-2 PDK-53 protein variant"

FT mutation replace(524, A)

FT /*tag= c

FT mutation replace(2055, C)

FT /*tag= d

FT mutation replace(2579, G)

FT /*tag= e

FT mutation replace(4018, C)

FT /*tag= f

FT mutation replace(5270, A)

FT /*tag= g

FT mutation replace(5547, T)

FT /*tag= h

FT mutation replace(6599, G)

FT /*tag= i

FT mutation replace(8571, C)

FT /*tag= j

XX WO200160847-A2.

PN 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07987.
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX Example 1; Page 276-292; 470pp; English.
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present CDNA
XX sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region
XX
SQ Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163
RESULT 22
ADN98025
ID ADN98025 standard; DNA; 10724 BP.
XX
XX AC ADN98025;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Dengue Virus isolate New Guinea complete genome sequence.
XX
XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX OS Dengue virus.
XX
XX PN WO2004040263-A2.
XX
XX PD 13-MAY-2004.
XX
XX PF 31-OCT-2003; 2003WO-US034823.
XX
XX PR 31-OCT-2002; 2002US-0422755P.
XX
XX PR 06-JUN-2003; 2003US-0476513P.
XX
XX PA (HEAL-) HEALTH RES INC.
XX

PI Wong SJ, Pei-Yong S;
XX WPI; 2004-400223/37.
XX
XX PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
XX reactive with antibody against WNV and cross-reactive with antibody
XX against a flavivirus, useful in diagnosing flavivirus infection caused by
XX DENV, WNV, JEV or SLEV.
XX
XX PS Disclosure; Fig 40; 212pp; English.
XX
XX CC The invention relates to a diagnostic kit comprising at least one
XX isolated and purified polypeptide comprising a West Nile Virus (WNV)
XX envelope (E) protein or its immunogenic fragment having a native
XX conformation or non-denatured structure and that is reactive with
XX antibodies against WNV and cross-reactive with antibodies against a
XX flavivirus. The diagnostic kit is useful in diagnosing flavivirus
XX infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
XX the complete nucleotide sequence of the DENV isolate New Guinea.
XX
SQ Sequence 10724 BP; 3542 A; 2212 C; 2725 G; 2245 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 12; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163
RESULT 23
AAD14609
ID AAD14609 standard; CDNA; 10756 BP.
XX
XX AC AAD14609;
XX
XX DT 11-SEP-2003 (revised)
XX
XX DT 06-AUG-2003 (revised)
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Dengue virus (DEN)-2/WN-PP1 chimeric CDNA.
XX
XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX OS Dengue virus; type II.
XX
XX OS West Nile virus.
XX
XX OS Chimeric.
XX
XX PH Key Location/Qualifiers
XX
XX FT CDS 97..10305
XX FT /*tag= a
XX FT /product= "DEN-2/WN-PP1 fusion protein"
XX
XX PN WO200160847-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 16-FEB-2001; 2001WO-US005142.
XX
XX PR 16-FEB-2000; 2000US-0182829P.
XX
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07988.
XX
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX

PS Example 6; Page 300-316; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/WN-PPI fusion protein related to the invention. This fusion protein contains DEN-2 16681 backbone and the premembrane/membrane protein (ppm) and an envelope protein (E) from West Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other; Query Match 100.0%; Score 28; DB 4; Length 10756; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 24
ADG93313
ID ADG93313 standard; DNA; 15159 BP.

XX AC ADG93313;
XX DT 11-MAR-2004 (first entry)
XX DE DEN2 (Tonga/74) cDNA plasmid P2.
XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
KW dengue virus; delta30; attenuating mutation; humoral response;
KW cellular response; non-structural protein; structural protein;
KW dengue virus serotype; gene; ds; plasmid P2.
XX OS Dengue virus type 2.
XX PN WO2003092592-A2.
XX PD 13-NOV-2003.
XX PF 25-APR-2003; 2003WO-US013279.
XX PR 03-MAY-2002; 2002US-0377860P.
XX PR 23-DEC-2002; 2002US-0436500P.
XX PA (USSS) US DEPT HEALTH & HUMAN SERVICES.
XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
PI Hanley K;
XX WPI; 2004-022612/02.
XX DR P-PSDB; ADG93314.
XX PT New tetravalent vaccine containing a common nucleotide deletion in the 3'
PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT of disease in humans caused by dengue virus, or for inducing immune
PT response.
XX PS Disclosure; SEQ ID NO 46; 181pp; English.
XX CC This invention relates to a novel immunogenic composition being
XX untranslanted region of dengue types 1, 2, 3, and 4, useful for preventing

CC This invention relates to a novel immunogenic composition being
CC tetravalent and containing a common nucleotide deletion in the 3'
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC structural proteins present in each dengue virus serotype. The present
CC invention is that of the DEN2 cDNA plasmid P2 which is related to the
CC invention.
XX SQ Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other; Query Match 100.0%; Score 28; DB 12; Length 15159; Best Local Similarity 100.0%; Pred. No. 0.016; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 25
ADG93317
ID ADG93317 standard; DNA; 2426 BP.

XX AC ADG93317;
XX DT 11-MAR-2004 (first entry)
XX DE DEN1 (Puerto Rico/94) CME chimeric region DNA SeqID50.
XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
KW dengue virus; delta30; attenuating mutation; humoral response;
KW cellular response; non-structural protein; structural protein;
KW dengue virus serotype; gene; ds; plasmid P2.
XX OS Dengue virus type 1.
XX PN WO2003092592-A2.
XX PD 13-NOV-2003.
XX PF 25-APR-2003; 2003WO-US013279.
XX PR 03-MAY-2002; 2002US-0377860P.
XX PR 23-DEC-2002; 2002US-0436500P.
XX PA (USSS) US DEPT HEALTH & HUMAN SERVICES.
XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
PI Hanley K;
XX WPI; 2004-022612/02.
XX DR P-PSDB; ADG93318.
XX PT New tetravalent vaccine containing a common nucleotide deletion in the 3'
PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT of disease in humans caused by dengue virus, or for inducing immune
PT response.
XX PS Disclosure; SEQ ID NO 50; 181pp; English.
XX CC This invention relates to a novel immunogenic composition being
XX tetravalent and containing a common nucleotide deletion in the 3'
XX untranslated region of dengue types 1, 2, 3, and 4. The invention may be
XX useful for the development of compounds with a virucide or

CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC) structural proteins present in each dengue virus serotype. The present
CC sequence is that of the DEN1 CME chimeric region DNA which is related to
CC the invention.

XX SQ Sequence 2426 BP; 754 A; 509 C; 632 G; 531 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 2426;

Best Local Similarity 96.4%; Pred. No. 0.066; Mismatches 1; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGCGAGAAACCGCG 28

Db 141 AATATGCTGAACCGCGAGAAACCGCG 168

RESULT 26

AAQ51476

ID AAQ51476 standard; DNA; 10718 BP.

XX AC AAQ51476;

XX DT 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 16-MAY-1994 (first entry)

XX DE DEN1-S275/90 (ECACC V92042111).

XX Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock syndrome;
KW DSS; DEN1 polypeptides; ss.

XX OS Dengue virus type 2.

XX FH Key Location/Qualifiers
XX CDS 81..10271

FT FT /*tag= a

FT FT 81..422

FT FT /*tag= b

FT FT /label= C

FT FT 123..422

FT FT /*tag= c

FT FT /label= C'

FT FT 423..695

FT FT /*tag= d

FT FT /label= Prem

FT FT 696..920

FT FT /*tag= e

FT FT /label= M

FT FT 921..2402

FT FT /*tag= f

FT FT /label= E

FT FT 2403..3464

FT FT /*tag= g

FT FT /label= NS1

FT FT 3465..4112

FT FT /*tag= h

FT FT /label= NS2A

FT FT 4113..4499

FT FT /*tag= i

FT FT /label= NS2B

FT FT 4500..6359

FT FT /*tag= j

FT FT /label= NS3

FT FT 6360..6809

FT FT /*tag= k

FT FT /label= NS4A

FT misc_RNA 6810..7556

FT FT /*tag= l

FT FT /label= NS4B

FT FT 7557..10268

FT FT /*tag= m

FT FT /label= NS5

XX PN WO9322440-A1.

XX PD 11-NOV-1993.

XX PF 28-APR-1993; 93WO-CA000182.

XX PR 29-APR-1992; 92GB-00009243.

XX PA (UYSI-) UNIV SINGAPORE NAT.

XX PI Tan Y, Pu J, Tan B, Yap E, Chan Y;

XX DR WPI; 1993-368799/46.

XX DR P-PSDB; AAR43662.

XX PT New Dengue virus type 1 strain - used to obtain prods. for detection,

XX diagnosis, vaccines and treatment involving virus.

XX PS Claim 3; Page 20-34; 55pp; English.

XX CC DEN1 virus, strain S275/90 was isolated from the serum of a dengue

XX CC haemorrhagic fever (DHF) patient. RNA was isolated from the virus and

XX CC used to prepare cDNA encoding DEN1 polypeptides. Dengue virus type 1

XX CC prods. can be used for detection, diagnosis, vaccines (inactivated form)

XX CC or treatment of DEN1 infections. The sequences given in AAQ51477-86 are

XX CC oligonucleotides used to prepare cDNA fragments corresp. to Dengue virus

XX CC proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.) (Updated

XX CC on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 10718 BP; 3419 A; 2226 C; 2769 G; 2304 T; 0 U; 0 Other;

XX Query Match 94.3%; Score 26.4; DB 2; Length 10718;

XX Best Local Similarity 96.4%; Pred. No. 0.08;

XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGCGAGAAACCGCG 28

Db 120 AATATGCTGAACCGCGAGAAACCGCG 147

RESULT 27

AAAD14603

ID AAAD14603 standard; cDNA; 10723 BP.

XX AC AAAD14603;

XX DT 11-SEP-2003 (revised)

XX DT 01-NOV-2001 (first entry)

XX DE Dengue virus (DEN)-2/1-VP chimeric cDNA.

XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;

XX KW immunogenic; viral disease; pharmaceutical; chimeric; ss.

XX OS Dengue virus; type I.

XX OS Dengue virus; type II.

XX OS Chimeric.

XX FH Key Location/Qualifiers

XX CDS 97..10272

FT FT /*tag= a

FT FT /product= "DEN-2/1-VP fusion protein"

XX PN WO200160847-A2.

XX PD 23-AUG-2001.

```
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07982.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 155-170; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), premembrane/membrane protein (prM) and an envelope
XX protein (E) from wild-type DEN-1 16007 virus. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
Best Local Similarity 96.4%; Pred. No. 0.08;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAAACCGCG 28
Db 136 AATATGCTGAACGCGGAGAAACCGCG 163

RESULT 28
AADI4604
ID AADI4604 standard; cDNA; 10723 BP.
XX
XX AADI4604;
XX
XX 11-SEP-2003 (revised)
XX 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VV chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
XX Dengue virus; type II.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 97..10272
XX /*tag= a
XX /product= "DEN-2/1-VV fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
```

```
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07983.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 179-195; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), premembrane/membrane protein (prM) and an envelope
XX protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10723 BP; 3514 A; 2228 C; 2722 G; 2259 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
Best Local Similarity 96.4%; Pred. No. 0.08;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAAACCGCG 28
Db 136 AATATGCTGAACGCGGAGAAACCGCG 163

RESULT 29
AADI4602
ID AADI4602 standard; cDNA; 10735 BP.
XX
XX AADI4602;
XX
XX 01-NOV-2001 (first entry)
XX
XX Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA.
XX
XX Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; mutein;
XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX ss.
XX
XX Dengue virus; type I.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 95..10273
XX /*tag= a
XX /product= "DEN-1 PDK-13 protein variant"
XX
XX mutation replace(1323, T)
XX mutation /*tag= b
XX mutation replace(1541, G)
XX mutation /*tag= c
XX mutation replace(1543, A)
```



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Db      134 AATATGCTGAACGCGGAGAAACCGG 161
RESULT 31
ADN98024
ID      ADN98024 standard; DNA; 10735 BP.
XX
AC      ADN98024;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Dengue Virus isolate WestPac complete genome sequence.
KW      ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
KW      Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
OS      Dengue virus.
XX
PN      WO2004040263-A2.
XX
PD      13-MAY-2004.
XX
PF      31-OCT-2003; 2003WO-US034823.
XX
PR      31-OCT-2002; 2002US-0422755P.
PR      06-JUN-2003; 2003US-0476513P.
XX
(HEAL-) HEALTH RES INC.
PA
PI      Wong SJ, Pei-Yong S;
XX
XX      WPI; 2004-400223/37.
DR
DR      GENBANK; U88535.
XX
XX      New diagnostic kit comprising West Nile Virus (WNV) envelope protein
PT      reactive with antibody against WNV and cross-reactive with antibody
PT      against a flavivirus, useful in diagnosing flavivirus infection caused by
PT      DENV, WNV, JEV or SLEV.
XX
XX      Disclosure; Fig 39; 212pp; English.
PS
XX
XX      The invention relates to a diagnostic kit comprising at least one
CC      isolated and purified polypeptide comprising a West Nile Virus (WNV)
CC      envelope (E) protein or its immunogenic fragment having a native
CC      conformation or non-denatured structure and that is reactive with
CC      antibodies against WNV and cross-reactive with antibodies against a
CC      flavivirus. The diagnostic kit is useful in diagnosing flavivirus
CC      infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
CC      the complete nucleotide sequence of the DENV isolate WestPac.
XX
XX      Sequence 10735 BP; 3421 A; 2245 C; 2774 G; 2295 T; 0 U; 0 Other;
SQ
Query Match          94.3%; Score 26.4; DB 12; Length 10735;
Best Local Similarity 96.4%; Pred. No. 0.08;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATATGCTGAACGCGGAGAAACCGG 28
      |||||
Db      134 AATATGCTGAACGCGGAGAAACCGG 161

RESULT 32
AAC68744
ID      AAC68744 standard; DNA; 26 BP.
XX
AC      AAC68744;
XX
DT      23-FEB-2001 (first entry)
XX
DE      Dengue virus type 2 upper primer.
XX
XX      Dengue virus; antiinflammatory; haemostatic; antibacterial; sepsis;
KW      immunosuppressive; immunomodulator; cardiac; cytostatic; cachexia;

KW      neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW      multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW      chronic myelogenous leukaemia; inflammatory bowel disease; PCR primer;
KW      ss.
XX
OS      Dengue virus.
XX
PN      WO200064479-A1.
XX
PD      02-NOV-2000.
XX
PF      26-APR-2000; 2000WO-US011700.
XX
PR      27-APR-1999; 99US-00301274.
XX
PA      (ANTI-) ANTIBODY SYSTEMS INC.
XX
PI      Fredeking TM, Ignatyev GM;
XX
XX      WPI; 2000-679646/66.
DR
XX
Novel compositions comprising tetracycline or tetracycline-like compounds
PT      for the treatment and/or prevention of acute inflammatory responses and
PT      diseases, e.g. septic shock and immune complex-induced colitis.
XX
XX      Example 2; Page 103; 183pp; English.
CC
XX      The present sequence was used in an invention relating to novel
CC      compositions and methods containing tetracycline or tetracycline-like
CC      compounds for treating and/or preventing acute inflammatory responses and
CC      diseases. Such diseases include acute inflammatory conditions associated
CC      with viral haemorrhagic diseases (including diseases caused by
CC      Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC      parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC      disorders, acute cardiovascular events, chronic myelogenous leukaemia and
CC      transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC      immune complex-induced colitis, cerebrospinal fluid inflammation,
CC      multiple sclerosis, inflammatory responses associated with trauma,
CC      systemic inflammatory response syndrome (SIRS), adult respiratory
CC      distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC      and Crohn's disease
XX
XX      Sequence 26 BP; 11 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match          92.9%; Score 26; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAACGCGGAGAAACCG 26
      |||||
Db      1 AATATGCTGAACGCGGAGAAACCG 26

RESULT 33
AAT75917
ID      AAT75917 standard; DNA; 28 BP.
XX
AC      AAT75917;
XX
DT      15-SEP-1997 (first entry)
XX
DE      DEN-2 cloning/sequencing sense primer, D2-134.
XX
XX      Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW      NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW      chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW      dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW      DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
XX
OS      Synthetic.
XX
XX      WO9640933-A1.
PN
XX

```

```

PD 19-DEC-1996.
XX
XX
PP 06-JUN-1996; 96WO-US009209.
XX
XX
PR 07-JUN-1995; 95US-00483292.
XX
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
DR
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Example; Page 100; 261pp; English.
XX
XX The sequences given in AAT75909-T76029 are primers which were used in the
CC amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the
CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises
CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.
CC The quadravalent vaccine of the invention comprises an attenuated Dengue
CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3
CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are
CC used to protect against infection by all four serotypes of dengue virus,
CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal
CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are
CC used to produce the recombinant protein products of the DNA constructs
CC which are used in the vaccines
XX
XX Sequence 28 BP; 11 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 92.9%; Score 26; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCG 26
Db 3 AATATGCTGAACGCGAGAGAAACCG 28

RESULT 34
AAD14610
ID AAD14610 standard; cDNA; 10699 BP.
XX
XX AAD14610;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-3 16562 cDNA.
XX
XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX Dengue virus; type III.
OS
XX
XX Key Location/Qualifiers
FH CDS 95..10267
FT /*tag= a
FT /product= "DEN-3 16562 protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX

(PSSH ) US DEPT HEALTH & HUMAN SERVICES.
PA Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;
XX
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07989.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 2; Page 325-341; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-3 (DEN-3) 16562 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10699 BP; 3437 A; 2224 C; 2779 G; 2259 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 4; Length 10699;
Best Local Similarity 92.9%; Pred. No. 0.42;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 134 AATATGCTGAACGCGTGAGAAACCGTG 161

RESULT 35
AAD14611
ID AAD14611 standard; cDNA; 10699 BP.
XX
XX AAD14611;
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX Attenuated, vaccine-strain DEN-3 PGMK-30/FRHL-3 variant cDNA.
XX
XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal; mutein;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
KW ss.
XX
XX Dengue virus; type III.
OS
XX
XX Key Location/Qualifiers
FH CDS 95..10267
FT /*tag= a
FT /product= "DEN-3 PGMK-30/FRHL-3 protein variant"
FT mutation replace(S50, C)
FT /*tag= b
FT mutation replace(1813, G)
FT /*tag= c
FT mutation replace(1838, A)
FT /*tag= d
FT mutation replace(1913, G)
FT /*tag= e

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```
PR 09-MAR-2001; 2001US-0274684P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA Pang X, Dayton AI, Zhang M;
XX WPI; 2002-723344/78.
XX
PT New subgenomic replicon of dengue virus origin comprising a deletion for
PT the sequence coding for C, PreM and/or E structural proteins, useful as
PT vaccines for immunization against dengue virus infection.
XX
PS Example 2; Page 38; 66pp; English.
XX
CC This invention describes a novel subgenomic replicon of dengue virus
CC origin comprising a deletion for the sequence coding for C, PreM and E
CC (DeltaCME), for PreM and E (DeltaME), or for E (DeltaE) structural
CC proteins, and/or which is adapted to receive at least a nucleotide
CC sequence without disrupting its replication capabilities. The products of
CC the invention can be used for constructing (1) a vaccine or a therapeutic
CC comprising the subgenomic replicon and a carrier; (2) a dengue virus-like
CC particle comprising the subgenomic replicon, and structural proteins of
CC the homologous dengue virus, which encapsulates the subgenomic replicon;
CC and (3) methods of immunisation and treatment comprising administering to
CC the individual the subgenomic replicon or the dengue virus like particle
CC cited above. The subgenomic replicons are useful in gene therapy as
CC vaccines for immunisation against dengue virus infection. This sequence
CC represents a PCR primer used with AAF8837 to amplify the green
CC fluorescent protein (GFP) gene cloned into the dengue virus delta-pre-M/E
CC replicon, at the site previously occupied by the pre-M/E genes
XX
SQ Sequence 72 BP; 26 A; 12 C; 24 G; 10 T; 0 U; 0 Other;
Query Match 78.6%; Score 22; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAA 22
DB 28 AATATGCTGAAACGCGAGAA 49
RESULT 40
ADR47008
ID ADR47008 standard; DNA; 96 BP.
XX
AC ADR47008;
XX
DT 18-NOV-2004 (first entry)
XX
DE Dengue virus vaccine oligonucleotide #1.
XX
KW ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
KW preM protein; C protein; NS1 protein signal; vaccine; cervical cancer;
KW viral disease; antigen; dendritic cell; immune response;
KW human papillomavirus.
XX
OS Unidentified.
XX
PN WO2004072274-A1.
XX
PD 26-AUG-2004.
XX
PF 30-JAN-2004; 2004WO-CN000088.
XX
PR 30-JAN-2003; 2003CN-00115272.
PR 30-JAN-2003; 2003CN-00115273.
XX
(PANG-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA (TENG-) TENGGEN BIOMEDICAL CO.
PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX
PI Pang X;
```

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XX WPI; 2004-625870/60.
XX
PT Virus-like particle vaccines containing dengue virus recombinant replicon
PT as core for carrier, applicable in preventives or/and remedies for tumors
PT like cervical cancer and viral diseases.
XX
PS Example 1; SEQ ID NO 5; 38pp; Chinese.
XX
CC A dengue virus recombinant replicon has a deletion of the complete coding
CC sequence for preM protein of dengue virus and also includes elements of
CC e.g. the non-coding region in the whole of the 5'-end, the coding region
CC of the front 20 amino acids in the C protein, and the coding region of
CC NS1 protein signal; coding regions of all non-structural proteins. The
CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to an oligonucleotide used in the
CC recombinant replicon of the invention.
XX
SQ Sequence 96 BP; 28 A; 20 C; 27 G; 21 T; 0 U; 0 Other;
Query Match 75.0%; Score 21; DB 13; Length 96;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGA 21
DB 25 AATATGCTGAAACGCGAGAGA 45
Search completed: July 31, 2005, 13:55:10
Job time : 234 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:00:46 ; Search time 1717.5 Seconds
(without alignments)
620.553 Million cell updates/sec

Title: US-10-085-944-2
Perfect score: 28
Sequence: 1 aatagctgaacggagagaaacgcg 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hnc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_ges1:*
- 9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	20.6	73.6	776	7	CF996467 AGENCOURT
C 2	19.8	70.7	720	7	CF455745 AGENCOURT
C 3	19.6	70.0	301	6	CB078143 h163h04.g
C 4	19.6	70.0	712	7	CF372439 CSECS052D
C 5	19.6	70.0	722	7	CF512147 Cabud0003
C 6	19.6	70.0	734	7	CF512236 Cabud0003
C 7	19.4	69.3	464	2	BE841207 QV4-SN002
C 8	19	67.9	520	9	CR305770 Medicago
C 9	19	67.9	541	7	CV235337 WS01218.B
C 10	19	67.9	559	9	TA262H01Q
C 11	19	67.9	568	8	AQ945692 Sheared D
C 12	19	67.9	576	9	TA140D12P
C 13	19	67.9	580	2	BE776235 MY-12-P-0
C 14	19	67.9	602	1	AL673619 AL673619
C 15	19	67.9	629	1	AL647632 AL647632
C 16	19	67.9	633	6	CA349616 620082 NC
C 17	19	67.9	649	6	CA356841 629106 NC
C 18	19	67.9	738	9	AG363192 Mus muscu
C 19	19	67.9	768	9	CC504335 CH240_344
C 20	19	67.9	870	9	AG186531 Pan trogl
C 21	19	67.9	988	7	CF995511 AGENCOURT
C 22	18.8	67.1	1687	2	BF128456 601810142
C 23	18.6	66.4	407	7	CF198531 EST0126 T
C 24	18.6	66.4	456	4	BG659286 TGESt2ya2

C	25	18.6	66.4	563	7	CF939381
C	26	18.6	66.4	584	8	AQ657703
C	27	18.6	66.4	593	9	FR0021761
C	28	18.6	66.4	636	7	CO300868
C	29	18.6	66.4	640	7	CN876173
C	30	18.6	66.4	642	1	AI135620
C	31	18.6	66.4	671	7	CN882707
C	32	18.6	66.4	675	7	CN879811
C	33	18.6	66.4	683	7	CN818097
C	34	18.6	66.4	684	8	AQ657387
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C	65	18.2	65.0	158	2	AW897358
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C	67	18.2	65.0	159	5	BQ345462
C	68	18.2	65.0	168	2	AW897370
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C	73	18.2	65.0	188	2	BF919968
C	74	18.2	65.0	192	2	BE763930
C	75	18.2	65.0	203	2	AW890996
C	76	18.2	65.0	211	1	AA364439
C	77	18.2	65.0	213	5	BQ340764
C	78	18.2	65.0	224	2	BF920089
C	79	18.2	65.0	232	2	BE763433
C	80	18.2	65.0	234	2	BF922730
C	81	18.2	65.0	242	2	BE764018
C	82	18.2	65.0	245	4	BI040884
C	83	18.2	65.0	248	5	BQ345780
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C	95	18.2	65.0	287	2	BF928047
C	96	18.2	65.0	287	2	BF763192
C	97	18.2	65.0	296	2	BF924560

98	18.2	65.0	299	1	AA338845	171	18.2	65.0	7	CK003909	CK003909	AGENCOURT
C 99	18.2	65.0	302	2	BF922613	172	18.2	65.0	616	7	CK003909	AGENCOURT
C 100	18.2	65.0	304	2	BF922609	173	18.2	65.0	617	5	BQ338598	QV4-N7025
C 101	18.2	65.0	309	2	BF933632	174	18.2	65.0	623	1	BQ338598	QV4-N7025
C 102	18.2	65.0	315	2	BF822307	175	18.2	65.0	629	4	BM688429	UI-E-CLO-
C 103	18.2	65.0	317	1	AA348826	176	18.2	65.0	629	7	CK002605	AGENCOURT
C 104	18.2	65.0	327	8	B62336	177	18.2	65.0	631	2	BF337960	60203794
C 105	18.2	65.0	327	8	B62336	178	18.2	65.0	633	4	BM686796	UI-E-CQO-
C 106	18.2	65.0	329	8	AQ020647	179	18.2	65.0	634	2	BF340047	602036986
C 107	18.2	65.0	330	1	AA371949	180	18.2	65.0	637	2	BF338164	602037966
C 108	18.2	65.0	333	1	AA348026	181	18.2	65.0	645	2	BF339643	602038923
C 109	18.2	65.0	348	1	AV709566	182	18.2	65.0	646	2	BF526151	602071053
C 110	18.2	65.0	349	5	BY068267	183	18.2	65.0	652	2	BF338165	602037967
C 111	18.2	65.0	351	4	BI041501	184	18.2	65.0	653	4	BG819424	602781667
C 112	18.2	65.0	353	2	BF922611	185	18.2	65.0	654	2	BF346112	602018660
C 113	18.2	65.0	355	1	AV420631	186	18.2	65.0	657	2	BF018697	ux97a05.x
C 114	18.2	65.0	355	1	BF944649	187	18.2	65.0	658	7	CK001828	AGENCOURT
C 115	18.2	65.0	355	5	BQ344497	188	18.2	65.0	664	2	BF526240	602071275
C 116	18.2	65.0	359	5	BQ345890	189	18.2	65.0	666	1	AJ451476	602038252
C 117	18.2	65.0	368	2	BF342880	190	18.2	65.0	670	2	BF340940	602038252
C 118	18.2	65.0	376	7	R87436	191	18.2	65.0	671	1	AV728966	AV728966
C 119	18.2	65.0	377	7	R87436	192	18.2	65.0	671	7	CR532392	CR532392
C 120	18.2	65.0	378	2	BF923985	193	18.2	65.0	672	4	BM702209	UI-E-CQ1-
C 121	18.2	65.0	378	7	H22054	194	18.2	65.0	676	2	BF525473	BF525473
C 122	18.2	65.0	381	1	AV709591	195	18.2	65.0	678	2	BF525884	602069844
C 123	18.2	65.0	386	9	AG226463	196	18.2	65.0	681	2	BF345694	602019336
C 124	18.2	65.0	387	1	AA321167	197	18.2	65.0	692	4	BM686457	UI-E-CRO-
C 125	18.2	65.0	387	4	BF960158	198	18.2	65.0	694	2	CK002568	AGENCOURT
C 126	18.2	65.0	392	2	BF933729	199	18.2	65.0	701	2	BF342433	602013937
C 127	18.2	65.0	393	6	CD613941	200	18.2	65.0	713	4	BG912875	602807455
C 128	18.2	65.0	395	6	CD613940	201	18.2	65.0	714	2	BF340186	602036562
C 129	18.2	65.0	400	7	H49669	202	18.2	65.0	717	2	BF340035	602036974
C 130	18.2	65.0	407	2	BF920871	203	18.2	65.0	719	4	BG819478	602781777
C 131	18.2	65.0	408	2	BF922617	204	18.2	65.0	720	1	AV726810	AV726810
C 132	18.2	65.0	408	2	BF933696	205	18.2	65.0	720	2	BF526793	602070345
C 133	18.2	65.0	411	2	BF920210	206	18.2	65.0	727	4	BG818708	602779024
C 134	18.2	65.0	413	2	BF936245	207	18.2	65.0	728	2	BF526512	602779024
C 135	18.2	65.0	420	4	BI041630	208	18.2	65.0	728	2	BF526684	602070520
C 136	18.2	65.0	431	4	BI041628	209	18.2	65.0	729	7	CF457105	AGENCOURT
C 137	18.2	65.0	431	7	H78082	210	18.2	65.0	729	7	CF457105	AGENCOURT
C 138	18.2	65.0	432	2	BF925437	211	18.2	65.0	748	4	BG914306	602812444
C 139	18.2	65.0	444	4	BI035799	212	18.2	65.0	748	2	BF341360	602013314
C 140	18.2	65.0	452	2	BF919956	213	18.2	65.0	750	1	AV727650	AV727650
C 141	18.2	65.0	466	2	BF922612	214	18.2	65.0	752	2	BF340044	602036983
C 142	18.2	65.0	470	2	BF922620	215	18.2	65.0	752	5	BX622852	BX622852
C 143	18.2	65.0	477	2	AW680872	216	18.2	65.0	754	2	CF457039	AGENCOURT
C 144	18.2	65.0	482	2	BF922601	217	18.2	65.0	755	2	BF337233	602035040
C 145	18.2	65.0	484	2	BF933707	218	18.2	65.0	757	2	BF341360	602013314
C 146	18.2	65.0	491	7	CF355594	219	18.2	65.0	757	2	CF453685	AGENCOURT
C 147	18.2	65.0	495	2	BF341915	220	18.2	65.0	761	7	CF453596	AGENCOURT
C 148	18.2	65.0	500	4	BM686644	221	18.2	65.0	762	7	CF453631	AGENCOURT
C 149	18.2	65.0	505	6	CB156658	222	18.2	65.0	762	7	CF453875	AGENCOURT
C 150	18.2	65.0	513	5	BQ345488	223	18.2	65.0	763	2	BF525554	602069656
C 151	18.2	65.0	527	5	BF215946	224	18.2	65.0	764	2	BF342632	602013773
C 152	18.2	65.0	533	2	BF526455	225	18.2	65.0	771	7	CF457181	AGENCOURT
C 153	18.2	65.0	538	2	BF699175	226	18.2	65.0	780	2	BF339990	602036922
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C 156	18.2	65.0	553	4	BM686618	229	18.2	65.0	784	7	CF456160	AGENCOURT
C 157	18.2	65.0	553	9	CNS03K5M	230	18.2	65.0	786	2	BF340178	602036553
C 158	18.2	65.0	556	2	BF924180	231	18.2	65.0	787	2	BF337199	602035003
C 159	18.2	65.0	560	4	BI038606	232	18.2	65.0	787	7	CF457398	AGENCOURT
C 160	18.2	65.0	567	2	BF343376	233	18.2	65.0	789	5	BX844416	BX844416
C 161	18.2	65.0	573	8	B2896076	234	18.2	65.0	789	7	CF456755	AGENCOURT
C 162	18.2	65.0	580	2	BF340973	235	18.2	65.0	791	2	BF340556	602037195
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C 164	18.2	65.0	581	4	BM686463	237	18.2	65.0	795	2	BF339025	602034813
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C 166	18.2	65.0	583	4	BM707034	239	18.2	65.0	796	4	CF456318	AGENCOURT
C 167	18.2	65.0	583	5	BF209711	240	18.2	65.0	798	4	BG912063	602809925
C 168	18.2	65.0	593	7	CF454482	241	18.2	65.0	801	2	BF339233	602038571
C 169	18.2	65.0	600	5	BQ636952	242	18.2	65.0	806	2	BF339062	602034855
C 170	18.2	65.0	613	2	BF342563	243	18.2	65.0	808	1	AL567923	AL567923

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245	18.2	65.0	815	2	BF525761	BF525761	602069903	C 318	18.2	65.0	1101	9	CNS05A5H	AL3280894 Tetraodon
246	18.2	65.0	821	2	BF344598	BF344598	602015219	C 319	18.2	65.0	1105	1	CNS05A5H	AL564810
247	18.2	65.0	825	2	BF342626	BF342626	602013764	320	18.2	65.0	1108	7	CF455877	CF455877 AGENCOURT
248	18.2	65.0	826	2	BF526276	BF526276	602071322	321	18.2	65.0	1108	7	BF526995	BF526995 602070275
249	18.2	65.0	827	7	CF455569	CF455569	602013722	322	18.2	65.0	1134	2	BF341690	BF341690 602016143
250	18.2	65.0	828	2	BF338209	BF338209	602037821	323	18.2	65.0	1144	2	BF344555	BF344555 602014968
251	18.2	65.0	830	2	BF338156	BF338156	602037957	324	18.2	65.0	1163	2	BF344849	BF344849 602014141
252	18.2	65.0	837	2	BF526348	BF526348	602070614	C 325	18.2	65.0	1246	5	BQ677481	BQ677481 AGENCOURT
253	18.2	65.0	840	1	AL564874	AL564874	602070614	C 326	18.2	65.0	1246	5	BQ677481	CR591619 full-leng
254	18.2	65.0	845	2	BF344620	BF344620	602015242	327	18.2	65.0	1336	3	CR685951	CR685951 Tetraodon
255	18.2	65.0	846	2	BF338284	BF338284	602035508	328	18.2	65.0	1706	2	BF341581	BF341581 602013595
256	18.2	65.0	846	4	BG818528	BG818528	602778752	329	18.2	65.0	1896	2	BF341513	BF341513 602013515
257	18.2	65.0	847	2	BF340808	BF340808	602037696	C 330	18.2	65.0	2116	4	BG852594	BG852594 1024034F0
258	18.2	65.0	852	2	BF343500	BF343500	602014613	C 331	18.2	65.0	2254	1	AV273660	AV273660 1024034F0
259	18.2	65.0	868	2	BF526131	BF526131	602071028	C 332	18.2	65.0	271	4	BF960356	BF960356 RCS-NN024
260	18.2	65.0	873	2	BF341029	BF341029	602038162	C 333	18.2	65.0	324	6	CA409632	CA409632 1173_F-P
261	18.2	65.0	874	2	BF343726	BF343726	602015384	334	18.2	65.0	352	1	AA590763	AA590763 vm21a02.r
262	18.2	65.0	875	2	BF525739	BF525739	602070072	C 335	18.2	65.0	409	9	FR0021804	AL014675 F.rubripe
263	18.2	65.0	876	2	BF340541	BF340541	602037178	C 336	18.2	65.0	432	1	AJ412375	AJ412375
264	18.2	65.0	879	2	BF342600	BF342600	602013732	C 337	18.2	65.0	549	9	TA353H02P	AL494474 T. Brucei
265	18.2	65.0	884	7	CF456336	CF456336	602036222	C 338	18.2	65.0	562	9	CL553485	CL553485 OB_Ha000
266	18.2	65.0	885	2	BF340899	BF340899	602038208	C 339	18.2	65.0	574	5	BU030479	BU030479 QHJ15110.
267	18.2	65.0	889	2	BF340517	BF340517	602037151	C 340	18.2	65.0	581	4	BM082773	BM082773 fu25903.Y
268	18.2	65.0	890	2	BF525917	BF525917	602069879	341	18.2	65.0	583	7	CO480568	CO480568 G00164.TB
269	18.2	65.0	892	2	BF341571	BF341571	602013580	342	18.2	65.0	597	9	FR0021765	AL014636 F.rubripe
270	18.2	65.0	895	2	BF338792	BF338792	602036222	343	18.2	65.0	598	4	BM867622	BM867622 mgc8010XF
271	18.2	65.0	896	2	BF340481	BF340481	602037107	C 344	18.2	65.0	627	4	BI509660	BI509660 BB170017A
272	18.2	65.0	898	2	BF338009	BF338009	602035887	345	18.2	65.0	636	6	CA969470	CA969470 CGLX06a22
273	18.2	65.0	899	2	BF340028	BF340028	602036967	346	18.2	65.0	650	6	BY738913	BY738913 BV738913
274	18.2	65.0	903	2	BF337815	BF337815	602035614	C 347	18.2	65.0	653	6	CB850104	CB850104 MRA-1865
275	18.2	65.0	904	2	BF343483	BF343483	602017587	348	18.2	65.0	659	5	BQ103758	BQ103758 ESTB1700
276	18.2	65.0	907	2	BF526612	BF526612	602070728	C 349	18.2	65.0	672	2	AW687277	AW687277 NF007H05R
277	18.2	65.0	904	2	BF341781	BF341781	602016287	C 350	18.2	65.0	672	2	AW687277	CG253787 OGICG94TH
278	18.2	65.0	910	2	BF342730	BF342730	602013685	351	18.2	65.0	679	8	BZ279852	BZ279852 CH230-308
279	18.2	65.0	913	2	BF338041	BF338041	602035929	C 352	18.2	65.0	705	9	CG438983	CG438983 QGVH024TH
280	18.2	65.0	914	1	AL566947	AL566947	602036947	C 353	18.2	65.0	712	1	AV760845	AV760845
281	18.2	65.0	916	2	BF338141	BF338141	602037937	C 354	18.2	65.0	734	5	AX879070	AX879070 BX879070
282	18.2	65.0	918	2	BF525533	BF525533	602069631	C 355	18.2	65.0	745	8	AQ854103	AQ854103 ndxb0053F
283	18.2	65.0	918	9	CG771201	CG771201	TGB50.4 G	C 356	18.2	65.0	752	9	CR132140	CR132140 Forward s
284	18.2	65.0	920	2	BF339188	BF339188	602038496	C 357	18.2	65.0	765	9	CG253787	CG253787 OGICG94TH
285	18.2	65.0	925	2	BF339656	BF339656	602038936	C 358	18.2	65.0	776	9	CR816616	CR816616 GR0AA41B
286	18.2	65.0	928	2	BF539140	BF539140	602038442	C 359	18.2	65.0	799	7	CF724220	CF724220 UT-M-GZ0
287	18.2	65.0	928	2	BF526123	BF526123	602071020	C 360	18.2	65.0	839	8	AZ187511	AZ187511 SF 1009.A
288	18.2	65.0	933	2	BF343464	BF343464	602017560	C 361	18.2	65.0	883	7	CR215227	CR215227 Forward s
289	18.2	65.0	946	7	CF456212	CF456212	602070870	C 362	18.2	65.0	921	9	CC700322	CC700322 QGVH024TH
290	18.2	65.0	949	2	BF338031	BF338031	602035917	C 363	18.2	65.0	948	9	CB589782	CB589782 AGENCOURT
291	18.2	65.0	950	2	BF343081	BF343081	602015708	C 364	18.2	65.0	959	6	CG854847	CG854847 PUIIK58TD
292	18.2	65.0	953	2	BF529034	BF529034	602040004	C 365	18.2	65.0	993	9	AG356625	AG356625 Mus muscu
293	18.2	65.0	954	2	BF526043	BF526043	602071148	C 366	18.2	65.0	1058	9	AG356625	CL647416 CH213-138
294	18.2	65.0	955	2	BF525936	BF525936	602070104	C 367	18.2	65.0	1080	9	CL647416	CL647416 CH213-15H
295	18.2	65.0	957	2	BF526560	BF526560	602070870	C 368	18.2	65.0	1163	9	AK040120	AK040120 Mus muscu
296	18.2	65.0	958	2	BF343797	BF343797	602015462	C 369	18.2	65.0	1211	3	AK040120	CL082979 ISB1-LD20
297	18.2	65.0	959	2	BF337322	BF337322	602034703	C 370	18.2	65.0	1214	9	CL082979	BI584713 RH23976.5
298	18.2	65.0	961	2	BF528370	BF528370	602043707	C 371	17.8	63.6	400	4	BI584713	BI584713 RH23976.5
299	18.2	65.0	964	5	BU485647	BU485647	603847639	C 372	17.8	63.6	453	4	BI574190	BI574190 RH22922.5
300	18.2	65.0	974	2	BF525632	BF525632	602069747	C 373	17.8	63.6	590	4	BI587424	BI587424 RH28096.5
301	18.2	65.0	977	2	BF339111	BF339111	602038411	C 374	17.8	63.6	592	4	BI631268	BI631268 RH60812.5
302	18.2	65.0	986	1	AL565650	AL565650	602069650	C 375	17.8	63.6	593	4	BI593544	BI593544 RH11641.5
303	18.2	65.0	987	8	CC297535	CC297535	CH261-105	C 376	17.8	63.6	598	4	BI584689	BI584689 RH23946.5
304	18.2	65.0	992	2	BF344521	BF344521	602014929	C 377	17.8	63.6	638	4	BI574629	BI574629 RH25930.5
305	18.2	65.0	1000	2	BF340220	BF340220	602036806	C 378	17.8	63.6	656	4	BI574556	BI574556 RH24493.5
306	18.2	65.0	1000	7	CF455859	CF455859	602036806	C 379	17.8	63.6	666	4	BI605401	BI605401 RH70993.5
307	18.2	65.0	1017	5	BX406938	BX406938	602069638	C 380	17.8	63.6	689	6	CA156073	CA156073 SCEPR2304
308	18.2	65.0	1032	2	BF339993	BF339993	602036926	C 381	17.8	63.6	694	4	BI586335	BI586335 RH26261.5
309	18.2	65.0	1034	2	BF525573	BF525573	602069679	C 382	17.8	63.6	694	8	BZ984187	BZ984187 PUGHK70TD
310	18.2	65.0	1042	2	AL532605	AL532605	602070320	C 383	17.8	63.6	848	7	CK308498	CK308498 SB02046BD
311	18.2	65.0	1065	1	BF344251	BF344251	602017313	C 384	17.8	63.6	852	8	BH658144	BH658144 BOMGT78TR
312	18.2	65.0	1069	2	BF344251	BF344251	602017313	C 385	17.8	63.6	925	2	BF340134	BF340134 602037296
313	18.2	65.0	1073	5	BM926332	BM926332	602014740	C 386	17.8	63.6	1186	4	BM019356	BM019356 603647513
314	18.2	65.0	1081	2	BF344362	BF344362	602014740	C 387	17.6	62.9	153	1	AV279194	AV279194 CM1-HT076
315	18.2	65.0	1083	2	BF525551	BF525551	602069652	C 388	17.6	62.9	240	2	BE716189	BE716189
316	18.2	65.0	1084	2	BF345568	BF345568	602019158	C 389	17.6	62.9	247	5	BQ698827	BQ698827 NXNV064F1

390	17.6	62.9	247	6	CD027812	CD027812 NXNV064F1	c	463	17.6	62.9	741	9	CG420304	CG420304 ZMMBBc003
391	17.6	62.9	290	2	BB086741	BB086741 BB086741	464	743	17.6	62.9	743	7	W25963	W25963 18a6 Human
c	392	17.6	318	2	BF824258	BF824258 NCST3a34	465	749	17.6	62.9	749	7	CK126720	CK126720 AGNCOURT
393	17.6	62.9	325	9	CR491666	CR491666 Medicago	c	466	17.6	62.9	763	9	CG050375	CG050375 PUJAL18TB
394	17.6	62.9	325	9	CG526041	CG526041 OST102148	467	763	17.6	62.9	763	8	BZ070651	BZ070651 lkk29a05
395	17.6	62.9	330	6	BY778929	BY778929 BY778929	468	772	17.6	62.9	772	8	BZ070651	BZ070651 lkk29a05
396	17.6	62.9	331	6	BY782961	BY782961 BY782961	469	781	17.6	62.9	781	7	CN991502	CN991502 68194_125
397	17.6	62.9	333	5	BY103109	BY103109 BY103109	470	783	17.6	62.9	783	7	CR189063	CR189063 GROAAA47B
398	17.6	62.9	347	5	BY062936	BY062936 BY062936	471	794	17.6	62.9	794	7	CO487831	CO487831 GQ0253b.B
c	399	17.6	353	7	CR521675	CR521675 CR521675	472	799	17.6	62.9	799	9	CR705245	CR705245 OGTAFJ51TM
400	17.6	62.9	367	5	BY066031	BY066031 BY066031	473	803	17.6	62.9	803	9	CR302929	CR302929 Medicago
c	401	17.6	367	5	BY066031	BY066031 BY066031	473	811	17.6	62.9	811	7	CO486932	CO486932 GQ0224.B7
402	17.6	62.9	397	2	AW920278	AW920278 Medicago	474	813	17.6	62.9	813	9	BX136279	BX136279 Danio rer
c	403	17.6	397	2	AW920278	AW920278 Medicago	475	840	17.6	62.9	840	9	CNS01EC9	ANopheles
404	17.6	62.9	397	6	CD026924	CD026924 NXNV017F0	c	476	17.6	62.9	863	9	CG705240	CG705240 OGTAFJ51TC
c	405	17.6	424	5	CA906548	CA906548 PCSC16023	477	872	17.6	62.9	872	7	CO815655	CO815655 AGNCOURT
406	17.6	62.9	424	5	CN631929	CN631929 taf45g02	c	478	17.6	62.9	879	7	CK202451	CK202451 FGA01097
407	17.6	62.9	425	5	BU012463	BU012463 QG31P22.Y	479	882	17.6	62.9	882	8	AQ576275	AQ576275 hxbx0088L
408	17.6	62.9	432	5	BY287560	BY287560 BY287560	480	895	17.6	62.9	895	9	CG207205	CG207205 OMBG34TH
c	409	17.6	436	7	CO104361	CO104361 GR_ED003	481	898	17.6	62.9	898	9	CG143486	CG143486 PUFUG70TD
c	410	17.6	436	7	CO104361	CO104361 GR_ED003	482	900	17.6	62.9	900	5	BU510337	BU510337 AGNCOURT
411	17.6	62.9	442	1	CN967169	CN967169 14666_100	483	917	17.6	62.9	917	7	CF823497	CF823497 EST700879
c	412	17.6	449	1	AV817480	AV817480 AV817480	484	919	17.6	62.9	919	6	CD501786	CD501786 CDA52-G05
c	413	17.6	459	2	BF060459	BF060459 NXCI_115	485	923	17.6	62.9	923	9	BX957902	BX957902 Forward s
c	414	17.6	460	1	A1548284	A1548284 UI-R-C3-E	486	937	17.6	62.9	937	9	CNS06SUI	AL413315 T3 end of
c	415	17.6	465	1	CD555686	CD555686 B0396C10-	487	942	17.6	62.9	942	9	CC713502	CC713502 OGBX70TV
c	416	17.6	479	9	BX991083	BX991083 Forward s	488	943	17.6	62.9	943	9	CG189837	CG189837 PUFVS27TB
c	417	17.6	491	2	BF232422	BF232422 UI-R-C3-E	489	954	17.6	62.9	954	4	BG343497	BG343497 HVSMEG000
c	418	17.6	497	1	AJ648532	AJ648532 AJ648532	490	960	17.6	62.9	960	9	CL229867	CL229867 T3 end of
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c	421	17.6	515	7	CO219541	CO219541 WS0107.B2	493	1010	17.6	62.9	1010	9	CNS05F63	CL283550 Tetraodon
c	422	17.6	519	5	BX254779	BX254779 BX254779	494	1011	17.6	62.9	1011	9	CL283550	CL283550 ZMMBB0062
c	423	17.6	525	8	AZ650113	AZ650113 1M0520A11	c	495	17.6	62.9	1093	5	BQ215270	BQ215270 AGNCOURT
c	424	17.6	533	4	BG146792	BG146792 mab95005	496	1094	17.6	62.9	1094	5	BQ215270	BQ215270 AGNCOURT
c	425	17.6	551	1	AL887606	AL887606 AL887606	c	497	17.6	62.9	1101	9	CNS05588	AL321716 Tetraodon
c	426	17.6	553	1	AL634615	AL634615 AL634615	c	498	17.6	62.9	1106	6	CD518550	CD518550 AGNCOURT
c	427	17.6	555	8	AQ589567	AQ589567 HS_2107.B	c	499	17.6	62.9	1112	6	CD505666	CD505666 CDA75-A01
c	428	17.6	555	8	AQ589567	AQ589567 HS_2107.B	c	500	17.6	62.9	1114	1	AV712153	AV712153 AV712153
c	429	17.6	586	9	CG965190	CG965190 MBEAP67TR								
c	430	17.6	588	9	CR333379	CR333379 Medicago								
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c	433	17.6	608	9	CR303333	CR303333 Medicago								
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c	435	17.6	615	7	CN981384	CN981384 43592_126								
c	436	17.6	618	3	CNS0A861	CNS0A861 Arabidops								
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c	460	17.6	698	8	BH983551	BH983551 Ode20g11								
c	461	17.6	703	5	BW257462	BW257462 BW257462								
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ALIGNMENTS

RESULT 1
CF996467/c
LOCUS CF996467.1 776 bp mRNA linear EST 25-NOV-2003
DEFINITION AGENCOURT_16394292 NIH_ZGC_7 Danio rerio cdna clone IMAGE:7037741
5', mRNA sequence.
ACCESSION CF996467
VERSION CF996467.1 GI:38517318
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 776)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Daniela S. Gerhard, Ph.D.
COMMENT Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cdna Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14788 row: e column: 03

-AUG-2003

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DEFINITION CSECS052D08_FLOn0012 CabSau Normalised Flower Stage 12 (FLOn0012)
Vitis vinifera cDNA clone CSECS052D08 3', mRNA sequence.
ACCESSION CF372439
VERSION CF372439.1 GI:34319685
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 712)
Iocco,P., Hua,C., Davies,C. and Thomas,M.R.
Expressed sequence tags from the grapevine cultivar Cabernet
Sauvignon
Contact: Mark R. Thomas
CSIRO Plant Industry
CSIRO
PO Box 350, Glen Osmond, SA, 5064, Australia
Tel: 61 8 83038600
Fax: 61 8 83038601
Email: Mark.R.Thomas@csiro.au
Seq primer: CCCAGTCACGAGCTGTAAACG (M13 Forward)
POLYA=yes.
FEATURES             source
    source
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        /mol_type="mRNA"
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        /db_xref="taxon:29760"
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        /dev_stage="12 - modified E-L system"
        /clone_lib="CabSau Normalised Flower Stage 12 (FLOn0012)"
        /note="Organ: Inflorescence including flowers; Vector:
        pZL; Normalised cDNA library from immature inflorescences
        at stage 12 of the modified E-L system. Tissue collected
        from field grown plants. A description of the modified E-L
        system can be found in the paper by B. G. Coombe 'Adoption
        of a system for identifying grapevine growth stages'
        (1995) Aust. J. Grape and Wine Res. 1: 104-110."
ORIGIN
Query Match          70.0%; Score 19.6; DB 7; Length 712;
Best Local Similarity 84.6%; Pred. No. 4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCG 26
    |||||
Db 374 ATTATGCTGAACCTCGAAGAAACTG 399

RESULT 5
CF512147/c
LOCUS CF512147.1 GI:34543915
DEFINITION Vitis vinifera
Bud - CABUD Vitis vinifera cv. Cabernet Sauvignon (Clone 8)
sequence.
ACCESSION CF512147
VERSION CF512147.1 GI:34543915
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 722)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
JOURNAL
COMMENT

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF512147
LOCUS CF512147.1 GI:34543915
DEFINITION Vitis vinifera
Bud - CABUD Vitis vinifera cv. Cabernet Sauvignon (Clone 8)
sequence.
ACCESSION CF512147
VERSION CF512147.1 GI:34543915
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 734)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
JOURNAL
COMMENT

```

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CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers
1..722
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    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon (Clone 8)"
    /db_xref="taxon:29760"
    /clone="CABUD0003_IF_A10"
    /sex="Hermaphrodite"
    /dev_stage="Pre-bloom (10-11 days before bloom)"
    /lab_host="DH5alpha"
    /clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone
    8) Bud - CABUD"
    /note="Organ: Bud; Vector: pDNR; Site 1: Sfil; Site 2:
    Sfil; CABUD is a cDNA library of Vitis vinifera cv.
    'Cabernet Sauvignon' Clone 8 dissected buds. Samples were
    collected May 13, 2002 from pre-bloom plants (10-11 days
    before bloom), pre-veraison. Sampled vines were located at
    the University of California, Davis, Experimental
    Vineyard. cDNAs were made by oligo-dT priming and
    directionally cloned. 5' and 3' adaptors were used in
    cloning as follows:
    5'-AGCAGTGGTATCAACGCGAGAGTGGCATTACGCGGG-3' and
    5'-ATTCTAGAGCCGAGCGCGACATG-3' Library was
    constructed using the Clontech Creator SMART kit and
    size-selected to contain the 0.5-3 kb size fraction."
ORIGIN
Query Match          70.0%; Score 19.6; DB 7; Length 722;
Best Local Similarity 84.6%; Pred. No. 4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCG 26
    |||||
Db 350 ACTATGCTGAACCTCGAAGAAACTG 325

RESULT 6
CF512236
LOCUS CF512236
DEFINITION Vitis vinifera
Bud - CABUD Vitis vinifera cDNA clone CABUD0003_IR_A10 3', mRNA
sequence.
ACCESSION CF512236
VERSION CF512236
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 734)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
JOURNAL
COMMENT

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF512236
LOCUS CF512236
DEFINITION Vitis vinifera
Bud - CABUD Vitis vinifera cDNA clone CABUD0003_IR_A10 3', mRNA
sequence.
ACCESSION CF512236
VERSION CF512236
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 734)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
JOURNAL
COMMENT

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF512236
LOCUS CF512236
DEFINITION Vitis vinifera
Bud - CABUD Vitis vinifera cDNA clone CABUD0003_IR_A10 3', mRNA
sequence.
ACCESSION CF512236
VERSION CF512236
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; Vitaceae; Vitis.
1 (bases 1 to 734)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
JOURNAL
COMMENT

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/clone="Cabud003_IR A10"
/sex="Hermaphrodite"
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/lab_host="DH5alpha"
/clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD"
/notes="Organ: Bud; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CABUD is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AGCAGTGGTATCAGCGAGAGTGGCCATTACGCCGG-3' and
5'-ATTCTAGCGCGAGCGCGGACATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Query Match 70.0%; Score 19.6; DB 7; Length 734;
Best Local Similarity 84.6%; Pred. No. 4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAACCG 26
Db 373 ACTATGCTGAACCTCGAAGAACTG 398

RESULT 7
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LOCUS BE841207 464 bp mRNA linear EST 22-SEP-2000
DEFINITION QV4-SN0024-200700-304-a07 SN0024 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE841207
VERSION BE841207.1 GI:10273585
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 464)
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldmann,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=QV4-SN0024-200700-304-a07&t3=2000-07-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 248.
Location/Qualifiers

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/notes="Organ: stomach normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 69.3%; Score 19.4; DB 2; Length 464;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TGCTGAACCGGAGAGAAC 25
Db 329 TGCTGAACCGGAGAGAAC 309

RESULT 8
CR305770
LOCUS CR305770 520 bp DNA linear GSS 01-MAR-2004
DEFINITION Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.
ACCESSION CR305770
VERSION CR305770.1 GI:44851914
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
REFERENCE 1 (bases 1 to 520)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
FEATURES
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/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
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Query Match 67.9%; Score 19; DB 9; Length 520;
Best Local Similarity 81.5%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAACCGC 27
Db 241 AACAGGCTGCAACGTGAAAGAAACCGC 267

RESULT 9
CV235337
LOCUS CV235337 541 bp mRNA linear EST 21-SEP-2004
DEFINITION WS01218.B21 L22 PT-GT-FL-A-3 Populus balsamifera subsp. trichocarpa cDNA clone WS01218_L22_3', mRNA sequence.
ACCESSION CV235337
VERSION CV235337.1 GI:52393807
KEYWORDS EST.

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[illegible]

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        /clone_lib="Sheared DNA"
        /note="Vector: pUC18; Site: 1: SmaI; Constructed at The
        Institute for Genomic Research (TIGR), Rockville, MD.
        Genomic DNA isolated from a cloned population of
        Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
        sheared to give a tight size distribution (approx 2 kb).
        The v + i method used for the library construction is
        described in detail in Smith, H.O. and Venter, J.C.
        (Making small insert libraries for whole genome shotgun
        sequencing projects. In Genome Sequencing: A Practical
        Approach, eds. M. Vaudin and B. Barrell, Oxford University
        Press, 1999)."

ORIGIN
  Query Match 67.9%; Score 19; DB 8; Length 568;
  Best Local Similarity 81.5%; Pred. No. 7.5e+02;
  Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGCAGAGAAACCGCG 28
  ||||| ||||| ||||| ||||| |||||
DB 415 ATATGCAGAAACGGCAGAGCAAGCAGC 389

RESULT 12
TAl40D12P 576 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 140d12, forward sequence,
genomic survey sequence.
AL466434 AL466434.1 GI:11835789
GSS.
||| ||||| ||||| ||||| |||||
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 576)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
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ORIGIN
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QY 2 ATATGCTGAAACGGCAGAGAAACCGCG 28
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DB 415 ATATGCAGAAACGGCAGAGCAAGCAGC 389

RESULT 12
TAl40D12P 576 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 140d12, forward sequence,
genomic survey sequence.
AL466434 AL466434.1 GI:11835789
GSS.
||| ||||| ||||| ||||| |||||
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 576)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
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ORIGIN
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  Best Local Similarity 81.5%; Pred. No. 7.5e+02;
  Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGCAGAGAAACCGCG 28
  ||||| ||||| ||||| ||||| |||||
DB 415 ATATGCAGAAACGGCAGAGCAAGCAGC 389

RESULT 12
TAl40D12P 576 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 140d12, forward sequence,
genomic survey sequence.
AL466434 AL466434.1 GI:11835789
GSS.
||| ||||| ||||| ||||| |||||
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 576)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
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QY 2 ATATGCTGAAACGGCAGAGAAACCGCG 28
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DB 415 ATATGCAGAAACGGCAGAGCAAGCAGC 389

RESULT 12
TAl40D12P 576 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 140d12, forward sequence,
genomic survey sequence.
AL466434 AL466434.1 GI:11835789
GSS.
||| ||||| ||||| ||||| |||||
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 576)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
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Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
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  Best Local Similarity 81.5%; Pred. No. 7.5e+02;
  Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGCAGAGAAACCGCG 28
  ||||| ||||| ||||| ||||| |||||
DB 415 ATATGCAGAAACGGCAGAGCAAGCAGC 389

RESULT 12
TAl40D12P 576 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 140d12, forward sequence,
genomic survey sequence.
AL466434 AL466434.1 GI:11835789
GSS.
||| ||||| ||||| ||||| |||||
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 576)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
  source
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ORIGIN
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  Best Local Similarity 81.5%; Pred. No. 7.5e+02;
  Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGCAGAGAAACCGCG 28
  ||||| ||||| ||||| ||||| |||||
DB 415 ATATGCAGAAACGGCAGAGCAAGCAGC 389

RESULT 12
TAl40D12P 576 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 140d12,
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REFERENCE
AUTHORS      1 (bases 1 to 602)
TITLE        Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
JOURNAL      Sanger Xenopus tropicalis EST project 2001 (11_2003)
COMMENT      Unpublished (2003)
              On Mar 18, 2002 this sequence version replaced gi:19529975.
              Contact: Taylor R
              Sanger Institute
              Hinxton, Cambridgeshire, CB10 1SA, UK
              Email: tropesanger.ac.uk
              This sequence is from a Xenopus Gene Collection (XGC) library
              constructed by Aaron M. Zorn.
              cDNA was oligo dt primed from Sug of poly A+ RNA from neurula.
              EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
              5' end and NotI at the 3' end.
              Vector: pCS107; Site_1: EcoRI; Site_2: NotI
              Host: Escherichia coli DH10B
              Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu062m06.plcSP6
Sequencing primer: SP6.
FEATURES
source
1..602
    /organism="Xenopus tropicalis"
    /mol_type="mRNA"
    /db_xref="taxon:8364"
    /clone="TNeu062m06"
    /dev_stage="neurula"
    /lab_host="Escherichia coli DH10B"
    /clone_lib="XGC-neurula"
    /notes="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
    was oligo dt primed from Sug of poly A+ RNA from neurula.
    EcoRI-NotI cut cDNA was then ligated into pCS107 with
    EcoRI at the 5' end and NotI at the 3' end."
ORIGIN
Query Match      67.9%; Score 19; DB 1; Length 602;
Best Local Similarity 81.5%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2 ATATGCTGAACGCGAGAGAAACCGCG 28
    ||| ||||| ||||| ||||| ||||| |||||
DB  202 ATAAGCTGAACGCGAGAGAAACGCG 228

RESULT 15
LOCUS      AL647632
DEFINITION AL647632 XGC-gastrula Xenopus tropicalis cDNA clone Tgas037f09 5',
mRNA sequence.
ACCESSION  AL647632.2 GI:38458607
VERSION     AL647632
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE   1 (bases 1 to 629)
AUTHORS     Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE       Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL     Unpublished (2003)
COMMENT     On Dec 13, 2001 this sequence version replaced gi:17655942.
              Contact: Huckle E
              Sanger Institute
              Hinxton, Cambridgeshire, CB10 1SA, UK
              Email: tropesanger.ac.uk
              This sequence is from a Xenopus Gene Collection (XGC) library
              constructed by Aaron M. Zorn.
              cDNA was oligo dt primed from Sug of poly A+ RNA from stages 10-13
              gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
              EcoRI at the 5' end and NotI at the 3' end.
              Vector: pCS107; Site_1: EcoRI; Site_2: NotI
              Host: Escherichia coli XLI-blue
              Sanger Xenopus tropicalis EST project 2001

TROPICALIS_SEQUENCE_ID: TGas037f09.plkSP6
Sequencing primer: SP6.
FEATURES
source
1..629
    /organism="Xenopus tropicalis"
    /mol_type="mRNA"
    /db_xref="taxon:8364"
    /clone="TGas037f09"
    /dev_stage="gastrula (stages 10.5-12 mixed)"
    /lab_host="Escherichia coli XLI-blue"
    /clone_lib="XGC-gastrula"
    /notes="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
    was oligo dt primed from Sug of poly A+ RNA from stages
    10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
    into pCS107 with EcoRI at the 5' end and NotI at the 3'
    end."
ORIGIN
Query Match      67.9%; Score 19; DB 1; Length 629;
Best Local Similarity 81.5%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2 ATATGCTGAACGCGAGAGAAACCGCG 28
    ||| ||||| ||||| ||||| ||||| |||||
DB  234 ATAAGCTGAACGCGAGAGAAACGCG 260

RESULT 16
LOCUS      CA349616
DEFINITION CA349616 633 bp mRNA linear EST 05-NOV-2002
5', mRNA sequence.
ACCESSION  CA349616.1 GI:24594787
VERSION     CA349616
KEYWORDS    EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1 (bases 1 to 633)
AUTHORS     Rexroad,C.E. 3rd, Lee,Y., Keele,J.W., Karamycheva,S., Brown,G.,
Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.
TITLE       Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
JOURNAL     Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
COMMENT     Contact: Rexroad CE
              USDA, ARS, National Center for Cool and Cold Water Aquaculture
              11876 Leetown Road, Kearneysville, WV 25430, USA
              Tel: 304 724 8340 x2129
              Fax: 304 725 0351
              Email: crexroad@cccwa.ars.usda.gov
              Single pass sequencing. Bases called with phred v0.020425.c and
              trimmed with the aid of the trim_al option. Vector identified by
              cross_match v0.990329.
              Seq primer: AGCGGATAACAATTTTCACACAGGA.
              Location/Qualifiers
              1..633
              /organism="Oncorhynchus mykiss"
              /mol_type="mRNA"
              /db_xref="taxon:8022"
              /clone="LRT142M04_C_G02"
              /tissue_type="pooled"
              /lab_host="DH10B"
              /clone_lib="NCCCWA 1RT"
              /notes="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
              Library made from pooled tissue from brain, gill, liver,
              spleen, muscle, and kidney."
ORIGIN
Query Match      67.9%; Score 19; DB 6; Length 633;
Best Local Similarity 81.5%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 ATATGCTGAACGCGAGAGAACCGC 27
Db 579 AATATGCAAGAACTGCGAGAGAACTGC 605

RESULT 17
CA356841
LOCUS 649 bp mRNA linear EST 05-NOV-2002
DEFINITION 629106 NCCWA lrt Oncorhynchus mykiss cdna clone lrt100m13_A.G07
ACCESSION 5', mRNA sequence.
CA356841
VERSION CA356841.1 GI:24602028
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Akiyama, T., Neopterygii; Teleostei; Euteleostei;
TITLE Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
JOURNAL 1 (bases 1 to 649)
COMMENT Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
 Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
 Sequence analysis of a rainbow trout cdna library and creation of a
 gene index
 Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
 Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified by
 cross_match v0.990329.
 Seq primer: AGCGGATAACAAATTTTCACACGGA.

FEATURES
 source
 1..649
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="lrt100m13_A.G07"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="NCCWA lrt"
 /notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from brain, gill, liver,
 spleen, muscle, and kidney."

ORIGIN
 Query Match 67.9%; Score 19; DB 6; Length 649;
 Best Local Similarity 81.5%; Pred. No. 7.5e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATATGCTGAACGCGAGAGAACCGC 27
Db 469 AATATGCAAGAACTGCGAGAGAACTGC 495

RESULT 18
AG363192/c
LOCUS 738 bp DNA linear GSS 03-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-164N14.TU, genomic survey
 sequence.
ACCESSION AG363192
VERSION AG363192.1 GI:47974397
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE BAC end Sequences of Library MSMg01

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 738)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
PRIMERS
 Sequencing : TJ
LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
FEATURES
 source
 1..738
 Location/Qualifiers
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-164N14.TJ"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
 Query Match 67.9%; Score 19; DB 9; Length 738;
 Best Local Similarity 81.5%; Pred. No. 7.6e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATATGCTGAACGCGAGAGAACCGC 27
Db 690 AATATACCGAAAGCGAGGAAAGCGC 664

RESULT 19
CC504335
LOCUS 768 bp DNA linear GSS 17-JUN-2003
DEFINITION CH240_344G2.T7 CHORI-240 Bos taurus genomic clone CH240_344G2,
 genomic survey sequence.
ACCESSION CC504335
VERSION CC504335.1 GI:31822628
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
REFERENCE 1 (bases 1 to 768)
AUTHORS Holt, R., Stott, J., Yang, G., Barber, S., Smalhus, D., Prabhu, A.-L.,
 Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
 Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
 Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
 Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,
 Dalrymple, B.P. and Tellam, R.
TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: CH240_344G2.TARBAC13P2
 Contact: Rob Holt
 Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bccsc.ca

Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering-information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.

Seq primer: T7

Plate: 344 row: G column: 2

Class: BAC ends.

Location/Qualifiers

1. .768
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_344G2"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull LI Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 768;
Best Local Similarity 81.5%; Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCGCG 28
|||||
DB 86 ATGTACAGAAACGTGAGAGAACCAACG 112
|||||

RESULT 20
AG186531/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-060P05.TJ, genomic survey
sequence.
ACCESSION AG186531
VERSION AG186531.1 GI:16716211
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 870)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Ageo Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (e-mail: chimbases@sc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. .870
/organism="Pan troglodytes"

FEATURES

source

/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-060P05.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 870;
Best Local Similarity 81.5%; Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCGCG 28
|||||
DB 690 ATATGCGAATCGCGAGAGCAACGCG 664
|||||

RESULT 21
CF995511/c
LOCUS
DEFINITION AGENCOURT 16028690 NIH_MGC.217 Homo sapiens cDNA clone
IMAGE:30524078 5', mRNA sequence.
ACCESSION CF995511
VERSION CF995511.1 GI:38512120
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 988)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>

Plate: NDAM603 row: a column: 15
High quality sequence stop: 407.

FEATURES

source

1. .988
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524078"
/cissue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 217"
/note="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI; Library is oligo-dT primed and directionally cloned. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. Average insert size 0.5-1kb. Adaptors 5'(AATTCGGCAGG)3' and 5'd (CTCGTGGCG)3'. 3' Linker sequence - GCGCGCTGAGAGCC T18. Sequencing primers 3'end: T3 promoter primer 5'd (ATTACCTCTCAAGGGA)3'. 5' End: T7 promoter primer 5'd (TAATACGACTCATATAGG)3'. Average insert size 0.5-1kb. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library."

ORIGIN


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Query Match      67.9%; Score 19; DB 7; Length 988;
Best Local Similarity 81.5%; Pred. No. 7.7e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGC 27
    ||||| ||||| ||||| |||||
Db 727 ATTATGCGGAACGAGAGATTACCGC 701

RESULT 22
BF128456      1687 bp mRNA linear EST 24-OCT-2000
LOCUS 601810142R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053059 3',
DEFINITION mRNA sequence.
ACCESSION BF128456
VERSION BF128456.1 GI:10967496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM891 row: c column: 12
High quality sequence start: 26
High quality sequence stop: 165.

FEATURES
source
1..1687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4053059"
/tissue_type="leiomyosarcoma cell line"
/lab_host="NIH10B (phage-resistant)"
/clone_lib="NIH MGC 46"
Notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match      67.1%; Score 18.8; DB 2; Length 1687;
Best Local Similarity 90.9%; Pred. No. 9.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAACGCGAGAGAAACCGC 28
    ||||| ||||| ||||| |||||
Db 694 CAGACACGCGAGAGAAACCGC 715

RESULT 23
CF198531/c      407 bp mRNA linear EST 01-AUG-2003
LOCUS EST0126 Tamarix androssowii leaf Tamarix androssowii cDNA, mRNA
DEFINITION sequence.
ACCESSION CF198531
VERSION CF198531.1 GI:33392904

KEYWORDS
SOURCE Tamarix androssowii
ORGANISM Tamarix androssowii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Tamaricaceae; Tamarix.
REFERENCE 1 (bases 1 to 407)
AUTHORS Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
TITLE EST acquired from cDNA library of Tamarix androssowii treated with
NaHCO3
JOURNAL Unpublished (2003)
COMMENT Contact: Yucheng Wang
Forestry Source and Environment College
Northeast Forestry University
Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
Tel: 086-451-2190607
Email: WANGYUCHENG1029@YAHOO.COM.CN.

FEATURES
source
1..407
/organism="Tamarix androssowii"
/mol_type="mRNA"
/db_xref="taxon:189785"
/tissue_type="leaf"
/clone_lib="Tamarix androssowii leaf"

ORIGIN
Query Match      66.4%; Score 18.6; DB 7; Length 407;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAAC 25
    ||||| ||||| ||||| |||||
Db 328 AATATGCTGAAGAGAGAGAAAC 304

RESULT 24
BG659286/c      456 bp mRNA linear EST 11-MAY-2001
LOCUS TgESTya21d01.y1 TgVEG118 Tachyzoite cDNA Library Toxoplasma gondii
DEFINITION cDNA clone TgESTya21d01.y1 5' similar to TR:O81505 O81505 F9D12.1
PROTEIN. ; mRNA sequence.
ACCESSION BG659286
VERSION BG659286.1 GI:13801535
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
REFERENCE 1 (bases 1 to 456)
AUTHORS Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajikwa, J.A., White, M.,
Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,
Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
Ritter, E., Bennett, J., Franklin, C., Tsagarishevili, R., Ronko, I.,
Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
TITLE Toxoplasma EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxos@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 408.

FEATURES
source
1..456
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"

```


Peterson, B. and Swimmer, C.
Exelixis FlyTag EST Project CK01 Library
Unpublished (2004)
Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: EK1795 row: E column: 4
High quality sequence stop: 467.

Location/Qualifiers
1. .636
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EK179552"
/clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and adult heads; Vector: pCDNA-SK+; Site 1: NotI; Site 2: XhoI; Random primed, normalized library from mixed stage embryos, imaginal disks, and adult heads."

Query Match 66.4%; Score 18.6; DB 7; Length 636;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAACCG 26
|||||
DB 205 ATATGCTGAACGCGAGAGAACCG 181
|||||

RESULT 29
CN876173
LOCUS
DEFINITION
x domestica cDNA clone AARA008897, mRNA sequence.
CN876173.1 GI:48262413
EST.
Malus x domestica (cultivated apple)
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 640)
Bennig, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

Location/Qualifiers
1. .640
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AARA008897"
/tissue_type="Leaf"
/dev_stage="Partially senescing leaf"
/clone_lib="(AARA) Royal Gala partially senescing leaf"
/note="Vector: pBK-CMV; Library sequenced by Genesis Research & Development"

Query Match 66.4%; Score 18.6; DB 7; Length 640;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;

QY 1 ANATGCTGAACGCGAGAGAACCG 25
|||||
DB 12 ANATGCTGAACGCGAAATRAACC 36
|||||

FR0021761
LOCUS
DEFINITION
F. rubripes GSS sequence, clone 067111bdl1, genomic survey sequence.
AL014632
AL014632.1 GI:2681000
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Takifugu.

1
Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J., Bouchireb, N., Cottage, A., Yeo, G.S., Umrانيا, Y., Williams, G. and Brenner, S.
Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
99455097
10523524
2 (bases 1 to 593)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrانيا, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgm.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic sequence.

Location/Qualifiers
1. .593
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="067111bdl1"
/clone_lib="cosmid 067111"

Query Match 66.4%; Score 18.6; DB 9; Length 593;
Best Local Similarity 80.8%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ANATGCTGAACGCGAGAGAACCG 26
|||||
DB 46 AANATGCTGAACGCGAGAGAGCG 71
|||||

CO300868
LOCUS
DEFINITION
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 636)
Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,

CO300868/c
LOCUS
DEFINITION
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 636)
Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 26
|||||

Db 43 ATATCTTGAAACGCGAGACGCTG 67
|||||

RESULT 30

LOCUS AI135620 642 bp mRNA linear EST 02-DEC-2003
DEFINITION GH13441.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH13441.5 similar to CG9322: FBan0009322
GO:[] located on: 3R 87F12-87F12.; 08/12/2002, mRNA sequence.

ACCESSION AI135620
VERSION AI135620.1 GI:3628178
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 642)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE BDGP/HMMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Other ESTs: GH13441.3prime
Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
hit genomic AE003701: arm:3R [9357746,9566163]
estimated-cyto:87F4-87F14: 04/10/2001
Plate: GH.134 row: D column: 5
High quality sequence stop: 593
POLYA=No.

FEATURES

source Location/Qualifiers
1..642
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="GH13441"
/sex="male and female"
/dev_stage="adult"
/lab_host="DHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site 1: EcoRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."

ORIGIN

Query Match 66.4%; Score 18.6; DB 1; Length 642;
Best Local Similarity 84.0%; Pred. No. 1.le+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 26
|||||

Db 191 ATATGCTGGAACGCGAGACGAG 215
|||||

RESULT 31

LOCUS CN882707 671 bp mRNA linear EST 04-JUN-2004
DEFINITION O10812AASB00315GHT (AASB) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASB003156, mRNA sequence.

ACCESSION CN882707
VERSION CN882707.1 GI:48268949
KEYWORDS EST.

SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1 (bases 1 to 671)
AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES source Location/Qualifiers
1..671
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AASB003156"
/tissue_type="Young fruit"
/dev_stage="10 days after full bloom"
/clone_lib="(AASB) Royal Gala 10 DAFB fruit"
/note="Vector: pBluescript SK(-); Library sequenced by
Genasis Research & Development"

ORIGIN
Query Match 66.4%; Score 18.6; DB 7; Length 671;
Best Local Similarity 84.0%; Pred. No. 1.le+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 26
|||||

Db 49 ATATCTGGAACGCGAGACGCTG 73
|||||

RESULT 32
LOCUS CN879811 675 bp mRNA linear EST 04-JUN-2004
DEFINITION O10419AASAO04412HT (AASA) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASAO04412, mRNA sequence.

ACCESSION CN879811
VERSION CN879811.1 GI:48266051
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1 (bases 1 to 675)
AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES source Location/Qualifiers
1..675
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AASAO04412"
/tissue_type="Fruit"
/dev_stage="10 days after full bloom"
/clone_lib="(AASA) Royal Gala 10 DAFB fruit"
/note="Vector: pBluescript SK(-); Library sequenced by
Genasis Research & Development"

ORIGIN
Query Match 66.4%; Score 18.6; DB 7; Length 671;
Best Local Similarity 84.0%; Pred. No. 1.le+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 26
|||||

Db 49 ATATCTGGAACGCGAGACGCTG 73
|||||

RESULT 32
LOCUS CN879811 675 bp mRNA linear EST 04-JUN-2004
DEFINITION O10419AASAO04412HT (AASA) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASAO04412, mRNA sequence.

ACCESSION CN879811
VERSION CN879811.1 GI:48266051
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1 (bases 1 to 675)
AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES source Location/Qualifiers
1..675
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AASAO04412"
/tissue_type="Fruit"
/dev_stage="10 days after full bloom"
/clone_lib="(AASA) Royal Gala 10 DAFB fruit"
/note="Vector: pBluescript SK(-); Library sequenced by
Genasis Research & Development"

Query Match 66.4%; Score 18.6; DB 7; Length 675;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGAGAGAAACCG 26
 |||||
 DB 60 ATATCTGAACCGAGAGACGCTG 84

RESULT 33
 LOCUS CN918097
 DEFINITION 030203ABPB004660HT (ABPB) M9 root tips Malus x domestica cDNA clone
 ABPB004660, mRNA sequence.
 CN918097
 ACCESSION CN918097
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Malus x domestica (cultivated apple)

REFERENCE 1 (bases 1 to 683)
 AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
 McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
 TITLE HortResearch Apple EST Project
 JOURNAL Unpublished (2004)
 COMMENT Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 Email: est@hortresearch.co.nz.

FEATURES
 source
 1..683
 /organism="Malus x domestica"
 /mol_type="mRNA"
 /db_xref="taxon:3750"
 /clone="ABPB004660"
 /tissue_type="Root tips (distal 1.5 cm)"
 /clone_lib="(ABPB) M9 root tips"
 /note="Vector: pBluescript SK(-); Library sequenced by
 Genesis Research & Development"

ORIGIN

Query Match 66.4%; Score 18.6; DB 7; Length 683;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACCGAGAGAAACCG 26
 |||||
 DB 1 ATATCTGAACCGAGAGACGCTG 25

RESULT 34
 LOCUS AO657387/c
 DEFINITION Sheared DNA-2N16.TR Sheared DNA Trypanosoma brucei genomic clone
 AO657387
 ACCESSION AO657387
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 684)
 AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
 Gerrard, C., Leech, V., de Jong, P., Ull, E., Melville, S.,
 Donelson, J., Fraser, C. and Adams, M.
 TITLE Determination of clone end sequences from Trypanosoma brucei GUTat

10.1 sheared DNA library
 Unpublished (1999)
 Other GSSs: Sheared DNA-2N16.TF
 Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: nelsayed@tigr.org
 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
 DNA library constructed at TIGR. Clones will be available for
 distribution through ATCC. Sheared DNA end sequences search page:
 http://www.tigr.org/cdb/mbd/tbdb/.
 Seq primer: M13-Reverse
 Class: shotgun.

FEATURES
 Location/Qualifiers
 1..684
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strains="TREU927/4 GUTat 10.1"
 /db_xref="taxon:5691"
 /clone="Sheared DNA-2N16"
 /clone_lib="Sheared DNA"
 /note="Vector: pUC18; Site 1: SmaI; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
 sheared to give a tight size distribution (approx 2 kb).
 The v + i method used for the library construction is
 described in detail in Smith, H.O. and Venter, J.C.
 (Making small insert libraries for whole genome shotgun
 sequencing projects. In Genome Sequencing: A Practical
 Approach, eds. M. Vaudin and B. Borell, Oxford University
 Press, 1999)."

ORIGIN

Query Match 66.4%; Score 18.6; DB 8; Length 684;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATATGCTGAACCGAGAGAAACCG 25
 |||||
 DB 548 ATATCTGAACCGAGAGAAACCG 524

RESULT 35
 LOCUS CL527496
 DEFINITION 83k06rp42.f1 RPCI-42 Bos taurus genomic clone 83k06rp42, genomic
 survey sequence.
 CL527496
 ACCESSION CL527496.1 GI:47120284
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Bos taurus (cow)

REFERENCE 1 (bases 1 to 799)
 AUTHORS Aycock, M.M., Najjar, F.Z., Gasbarre, L.C., Van Tassel, C.P.,
 Sonstegard, T.S., Conner, E.E., Capuco, A.V. and Roe, B.A.
 TITLE Bovine BAC End Sequences from RPCI-42 Library
 JOURNAL Unpublished (2004)
 COMMENT Contact: Bruce A. Roe
 Advanced Center for Genome Technology
 University of Oklahoma Department of Chemistry and Biochemistry
 620 Parrington Oval, Room 208, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Class: BAC ends
 High quality sequence start: 133

High quality sequence stop: 524.

FEATURES
source
1. .799
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Holstein Bull"
/db_xref="taxon:9913"
/clone="83k06rp42"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match 66.4%; Score 18.6; DB 9; Length 799;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATATGCTGAAGCGGAGAGAACCAGC 28
|||||
Db 63 AGTAGNCNGAACGGCCGAGAAAACCAACG 90
|||||

RESULT 36
LOCUS CG016439 427 bp DNA linear GSS 19-AUG-2003
DEFINITION ZUAAG30TH ZM 3.0 4.0 KB Zea mays genomic clone ZMMBPaa0006E11,
genomic survey sequence.
ACCESSION CG016439 GI:33888604
VERSION GSS.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 427)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: ZUAAG30TV
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1. .427
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBPaa0006E11"
/clone_lib="ZM 3.0 4.0 KB"
/notes="Vector: pBGSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"

ORIGIN
Query Match 65.7%; Score 18.4; DB 9; Length 427;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAGCGGAGAGAACCAGC 28
|||||
Db 332 AATATGCTGAAGCGGTAGAGAGGCCG 359
|||||

RESULT 37
LOCUS AO724090/c 456 bp DNA linear GSS 14-JUL-1995
DEFINITION HS_5375_A2 H09_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=951 Col=18 Row=O, genomic survey sequence.
ACCESSION AO724090
VERSION AO724090.1 GI:5483759
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 456)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3687
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pietere@jmg.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
<http://www.htsec.washington.edu>
Plate: 951 row: O column: 18
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 456.
Location/Qualifiers
1. .456
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=951 Col=18 Row=O"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methyllase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 65.7%; Score 18.4; DB 8; Length 456;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAGCGGAGAGAACCAGC 28
|||||
Db 300 AATGTGATTACAGCGGTGAGAAACCGC 273
|||||

RESULT 38
LOCUS AWS99272 496 bp mRNA linear EST 22-MAR-2000
DEFINITION gbl2g03.y1 Moss EST library PPN Physcomitrella patens cDNA clone
PEP SOURCE ID:PPN091205 5' similar to WP:C33F10.3 CE02530 E. COLI
ORF_F226\; YEAST YJ4 PROTEIN i, mRNA sequence.
ACCESSION AWS99272
VERSION AWS99272.1 GI:7286785
KEYWORDS EST.
SOURCE Physcomitrella patens
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
Brvoisida; Funariidae; Funariales; Funariaceae; Physcomitrella.

1 (bases 1 to 496)
Quatrano, R., Bashardes, S., Cove, D., Cumming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wyllie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
Leeds/Wash U Moss EST Project
Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Gibco
High quality sequence stop: 416.
Location/Qualifiers
1..496
/organism="Physcomitrella patens"
/mol_type="mRNA"
/db_xref="taxon:3218"
/clone="PEP SOURCE ID: PPN091205"
/tissue_type="protonemata: 7 day old tissue auxin treated"
/lab_host="DH10B"
/clone_lib="Moss EST library PPN"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Construction of the cDNA library was carried out using Stratagene's 'UniZAP' - cDNA synthesis kit'. cDNA was constructed using an oligo dt primer/linker that contains a XhoI site within it. Following ds cDNA synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with XhoI. The result is cDNA with an EcoRI sticky end on one side and a XhoI sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold gigapackaging extracts. Library was grown in XL1Blue MRF' cells and amplified. The library was excised by mass excision using Stratagene's 'Mass excision kit' that uses exasist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cells as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered. The double stranded plasmid library was recovered by using Qbiogen Midi prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."

REFERENCE
AUTHORS
Quatrano, R., Bashardes, S., Cove, D., Cumming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wyllie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
Unpublished (1999)
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Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Gibco
High quality sequence stop: 416.
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/organism="Physcomitrella patens"
/mol_type="mRNA"
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Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL2 PCR based library. cDNA PCR products of size >400 nucleotides containing SL2 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Intestine RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu).
Seq primer: SL1 primer
High quality sequence stop: 525.

FEATURES
source

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ORIGIN

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Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 264 ATTTGCTGATGCGCGAGAGAAACCGCG 291

Search completed: July 31, 2005, 13:48:06
Job time : 1740.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:23:11 ; Search time 71.5 Seconds
(without alignments)
640.780 Million cell up

Title: US-10-085-944-2

Perfect score: 28
Sequence: 1 aatatgctgaaacgcgagagaaaccgcg 28

Scoring table: IDENTITY NUC

Gapop 10⁻⁰ , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Post-processing: Minimum

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	100.0	3381	3	US-08-937-195-1		Sequence 2, Appli
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4	28	100.0	3381	3	US-08-915-152-1		Sequence 2, Appli
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c 134	16	57.1	1428	4	US-09-583-110-1666	Sequence 1666, App	c 207	15.8	56.4	3569	4	US-09-710-279-4443	Sequence 4443, App
c 135	16	57.1	1431	4	US-09-107-433-475	Sequence 475, App	c 208	15.8	56.4	4297	4	US-09-710-279-4092	Sequence 4092, App
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c 137	16	57.1	2010	4	US-09-902-540-9547	Sequence 9547, App	c 210	15.8	56.4	4860	4	US-09-949-016-2961	Sequence 2961, App
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c 146	16	57.1	19446	3	US-08-961-527-51	Sequence 51, Appl	c 219	15.8	56.4	5890	5	PCT-US93-07347-3	Sequence 3, Appl
c 147	16	57.1	27630	4	US-09-949-016-12722	Sequence 12722, A	c 220	15.8	56.4	5890	5	PCT-US93-07347-5	Sequence 5, Appl
c 148	16	57.1	81001	3	US-09-750-580-1	Sequence 1, Appl	c 221	15.8	56.4	5890	5	PCT-US93-07347-6	Sequence 6, Appl
c 149	16	57.1	89047	4	US-09-596-002-34	Sequence 34, Appl	c 222	15.8	56.4	6295	1	US-08-003-311B-4	Sequence 4, Appl
c 150	16	57.1	109025	4	US-09-949-016-12609	Sequence 12609, A	c 223	15.8	56.4	6295	1	US-08-261-432-4	Sequence 4, Appl
c 151	16	57.1	109025	4	US-09-949-016-17567	Sequence 17567, A	c 224	15.8	56.4	6312	1	US-08-003-311B-3	Sequence 3, Appl
c 152	16	57.1	128779	4	US-09-497-855A-38	Sequence 38, Appl	c 225	15.8	56.4	6312	1	US-08-003-311B-5	Sequence 5, Appl
c 153	16	57.1	135030	4	US-09-949-016-14896	Sequence 14896, A	c 226	15.8	56.4	6312	1	US-08-003-311B-6	Sequence 6, Appl
c 154	16	57.1	181251	4	US-09-949-016-15970	Sequence 15970, A	c 227	15.8	56.4	6312	1	US-08-003-311B-7	Sequence 7, Appl
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c 156	16	57.1	198637	4	US-09-949-016-17393	Sequence 17393, A	c 229	15.8	56.4	6312	1	US-08-261-432-5	Sequence 5, Appl
c 157	16	57.1	247781	4	US-09-949-016-14193	Sequence 14193, A	c 230	15.8	56.4	6312	1	US-08-261-432-6	Sequence 6, Appl
c 158	16	57.1	254366	4	US-09-822-871-3	Sequence 3, Appl	c 231	15.8	56.4	6312	1	US-08-261-432-7	Sequence 7, Appl
c 159	16	57.1	786431	4	US-09-751-369-3	Sequence 3, Appl	c 232	15.8	56.4	9335	4	US-09-502-540-940	Sequence 940, App
c 160	16	57.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl	c 233	15.8	56.4	11271	4	US-08-956-171E-11	Sequence 11, Appl
c 161	16	57.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl	c 234	15.8	56.4	11271	4	US-08-781-986A-11	Sequence 11, Appl
c 162	15.8	56.4	190	4	US-09-513-999C-10050	Sequence 10050, A	c 235	15.8	56.4	12368	3	US-08-976-259-20	Sequence 20, Appl
c 163	15.8	56.4	405	4	US-09-710-279-3005	Sequence 3005, App	c 236	15.8	56.4	12368	4	US-09-956-004-20	Sequence 14148, A
c 164	15.8	56.4	405	4	US-09-710-279-3045	Sequence 3045, App	c 237	15.8	56.4	15100	4	US-09-949-016-17168	Sequence 17168, A
c 165	15.8	56.4	405	4	US-09-710-279-3303	Sequence 3303, App	c 238	15.8	56.4	28129	4	US-09-949-016-17169	Sequence 17169, A
c 166	15.8	56.4	423	4	US-09-270-767-7033	Sequence 7033, App	c 239	15.8	56.4	31820	4	US-09-949-016-13356	Sequence 13356, A
c 167	15.8	56.4	423	4	US-09-270-767-22315	Sequence 22315, A	c 240	15.8	56.4	31820	4	US-09-949-016-17609	Sequence 17609, A
c 168	15.8	56.4	520	4	US-09-621-976-811	Sequence 811, App	c 241	15.8	56.4	47110	4	US-09-949-016-11867	Sequence 11867, A
c 169	15.8	56.4	573	4	US-09-270-767-126	Sequence 126, App	c 242	15.8	56.4	48536	4	US-09-949-016-17167	Sequence 17167, A
c 170	15.8	56.4	573	4	US-09-270-767-15408	Sequence 15408, A	c 243	15.8	56.4	48536	4	US-09-949-016-17167	Sequence 17167, A
c 171	15.8	56.4	601	4	US-09-949-016-20277	Sequence 20277, A	c 244	15.8	56.4	66219	4	US-09-949-016-12038	Sequence 12038, A
c 172	15.8	56.4	601	4	US-09-949-016-24007	Sequence 24007, A	c 245	15.8	56.4	66219	4	US-09-949-016-12038	Sequence 12038, A
c 173	15.8	56.4	601	4	US-09-949-016-14192	Sequence 14192, A	c 246	15.8	56.4	84171	4	US-09-949-016-16356	Sequence 16356, A

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248	15.8	56.4	87563	3	US-09-453-702B-57	Sequence 57, Appl	C 321	15.6	55.7	1830121	4	US-09-643-990A-1	Sequence 1, Appli
C 249	15.8	56.4	113283	4	US-09-949-016-16976	Sequence 16976, A	C 322	15.4	55.0	98	4	US-09-513-999C-27844	Sequence 27844, A
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C 257	15.8	56.4	147321	4	US-09-949-016-15450	Sequence 15450, A	C 330	15.4	55.0	344	4	US-09-513-999C-21564	Sequence 21564, A
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C 259	15.8	56.4	150409	4	US-09-949-016-12938	Sequence 12938, A	C 332	15.4	55.0	360	4	US-09-489-039A-3102	Sequence 3102, Ap
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C 262	15.6	55.7	601	4	US-09-949-016-66060	Sequence 66060, A	C 335	15.4	55.0	462	4	US-09-573-080A-249	Sequence 249, App
C 263	15.6	55.7	601	4	US-09-949-016-79456	Sequence 79456, A	C 336	15.4	55.0	468	4	US-09-328-352-935	Sequence 935, App
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C 274	15.6	55.7	1023	4	US-09-940-244-401	Sequence 401, App	C 347	15.4	55.0	601	4	US-09-949-016-129186	Sequence 129186, A
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C 285	15.6	55.7	5822	3	US-08-899-595-4	Sequence 4, Appli	C 358	15.4	55.0	773	1	US-07-789-738-5	Sequence 5, Appli
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C 289	15.6	55.7	26684	4	US-09-949-016-15109	Sequence 15109, A	C 362	15.4	55.0	936	4	US-09-252-991A-14805	Sequence 14805, A
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C 293	15.6	55.7	31096	4	US-08-956-171B-59	Sequence 59, Appl	C 366	15.4	55.0	1147	4	US-09-721-341-1	Sequence 1, Appli
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C 309	15.6	55.7	205044	4	US-09-949-016-15853	Sequence 15853, A	C 382	15.4	55.0	1564	4	US-09-270-767-14725	Sequence 14725, A
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C 313	15.6	55.7	285986	4	US-09-949-016-12287	Sequence 12287, A	C 386	15.4	55.0	1830	4	US-09-107-532A-1536	Sequence 1536, Ap
C 314	15.6	55.7	288031	4	US-09-949-016-14864	Sequence 14864, A	C 387	15.4	55.0	1836	4	US-09-328-352-1536	Sequence 1536, Ap
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C 316	15.6	55.7	784019	4	US-09-949-016-14033	Sequence 14033, A	C 389	15.4	55.0	2363	4	US-09-949-016-2159	Sequence 2159, Ap
C 317	15.6	55.7	828152	4	US-09-949-016-12777	Sequence 12777, A	C 390	15.4	55.0	2505	4	US-09-614-221A-73	Sequence 73, Appl
C 318	15.6	55.7	1230025	4	US-09-198-452A-1	Sequence 1, Appli	C 391	15.4	55.0	2625	3	US-09-453-702B-210	Sequence 210, App
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: New Guinea C
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Prem and Envelope
MAP POSITION: 330-2446
UNITS: bp
PUBLICATION INFORMATION:
AUTHORS: Gruenberg, A
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AUTHORS: Wright, P J
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TITLE: acid sequence of the structural proteins of dengue
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AUTHORS: Irie, K
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Db 60 AATATGCTGAACCGGAGAGAAACCGCG 87
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RESULT 2

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Sequence 1, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: misc_feature
LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the S1 strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= (1).
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1218
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1260
OTHER INFORMATION: /note= "T is replaced by G for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1929

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; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
; US-08-937-195-1
;
; Query Match 100.0%; Score 28; DB 3; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.0029;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGGAGAGAACCGG 28
;
; Db 40 AATATGCTGAACCGGAGAGAACCGG 67
;
; RESULT 3
; US-08-937-195-2
; Sequence 2, Application US/08937195
; Patent No. 6136561
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937.195
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2(DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
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CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: misc_feature
LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the S1 strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1218_
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1260_
OTHER INFORMATION: /note= "T is replaced by G for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762_
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1929_
OTHER INFORMATION: /note= "C is replaced by T for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2310_
OTHER INFORMATION: /note= "A is replaced by N for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1_
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343_
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616_
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841_
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326_
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-915-152-1
Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
Db 40 AATATGCTGAAACCGGAGAGAAACCGCG 67

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RESULT 5
US-08-915-152-2
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
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; OTHER INFORMATION: strain(citation #1)"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-2
;
; Query Match 100.0%; Score 28; DB 3; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.0029;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | | | |
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67
| | | | | | | | | | | | | | | | | | | |
;
RESULT 6
US-09-376-463-2
; Sequence 2, Application US/09376463
; Patent No. 6749857
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; FILE REFERENCE: 24733-20005.20
; CURRENT APPLICATION NUMBER: US/09/376,463
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
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; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-09-376-463-2
Query Match      100.0%; Score 28; DB 4; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 7
PCT-US96-07627-1
; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-1

Query Match      100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 8
PCT-US96-07627-2
; Sequence 2, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1782..1784
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; PCT-US96-07627-2
;
; Query Match 100.0%; Score 28; DB 5; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.0029;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
; Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
;
; RESULT 9
; US-08-325-426B-1
; Sequence 1, Application US/08325426B
; Patent No. 6017535

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; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
; US-08-325-426B-1
;
; Query Match 94.3%; Score 26.4; DB 3; Length 10718;
; Best Local Similarity 96.4%; Pred. No. 0.02;
; Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
; Db 120 AATATGCTGAACCGGAGAGAAACCGCG 147
;
; RESULT 10
; US-09-270-767-9819/c
; Sequence 9819, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9819
; LENGTH: 1145
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-9819
;
; Query Match 66.4%; Score 18.6; DB 4; Length 1145;
; Best Local Similarity 84.0%; Pred. No. 50;
; Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 2 ATATGCTGAACGCGAGAGAAACCG 26
Db 452 ATATGCTGAACGCGAGAGAAACCG 428

RESULT 11
US-09-078-173A-11
; Sequence 11, Application US/09078173A
; Patent No. 6200794
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Braah
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-09-078-173A-11

Query Match 65.7%; Score 18.4; DB 3; Length 1443;
Best Local Similarity 78.6%; Pred. No. 64;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 933 AAAATGCTGAGATCAAGAGAACTGAG 960

RESULT 12
US-10-042-991-11
; Sequence 11, Application US/10042991
; Patent No. 6780621
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Braah
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE REFERENCE: 06027.0001U3
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match 65.7%; Score 18.4; DB 4; Length 1443;
Best Local Similarity 78.6%; Pred. No. 64;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 933 AAAATGCTGAGATCAAGAGAACTGAG 960

RESULT 13
US-08-224-391-52
; Sequence 52, Application US/08224391
; Patent No. 5744140

; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-224-391-52

Query Match 65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 81;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 43 AATATGCTGAACGCGGCTTATCCCGCG 70

RESULT 14
US-08-484-304-52
; Sequence 52, Application US/08484304
; Patent No. 5744141
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,304
```

```
;
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-484-304-52
;
Query Match 65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 81;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
Db 43 AATATGCTGAACGCGGCTTACCCCGCG 70

RESULT 15
US-08-811-566-5/c
; Sequence 5, Application US/08811566
; Patent No. 6127116
; GENERAL INFORMATION:
; APPLICANT: Rice, Charles et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,566
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1113-1-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-811-566-5
```

```
US-08-811-566-5
;
Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 16
US-09-034-756-5/c
; Sequence 5, Application US/09034756
; Patent No. 6392028
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,756
; FILING DATE: 04-May-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
;
US-09-034-756-5
;
Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 17
US-09-949-016-23984/c
; Sequence 23984, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23984
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23984

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 87.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 29 AAGATGCTGAAACGCGAGAGAAA 7

RESULT 18

US-09-949-016-91406/c
; Sequence 91406, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91406
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-91406

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 87.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 104 AATATGCTGAATGCGATAAAA 82

RESULT 19

US-09-949-016-127192/c
; Sequence 127192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127192
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-127192

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 87.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 29 AAGATGCTGAAACGCGAGAGAAA 7

RESULT 20

US-09-949-016-3621
; Sequence 3621, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3621
; LENGTH: 3029
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3621

Query Match 65.0%; Score 18.2; DB 4; Length 3029;
Best Local Similarity 87.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 2399 AAGATGCTGAAACGCGAGAGAAA 2421

RESULT 21

US-09-949-016-295
; Sequence 295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 295
; LENGTH: 3033
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-295

Query Match          65.0%; Score 18.2; DB 4; Length 3033;
Best Local Similarity 87.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAA 23
Db 2398 AAGATGCTGAACACAGGAGAGAAA 2420
      |||||
RESULT 22
US-09-949-016-12037
; Sequence 12037, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12037
; LENGTH: 13871
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12037

Query Match          65.0%; Score 18.2; DB 4; Length 13871;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAA 23
Db 11241 AAGATGCTGAACACAGGAGAGAAA 11263
      |||||
RESULT 23
US-09-949-016-15363
; Sequence 15363, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15363
; LENGTH: 13871
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15363
```

```
Query Match          65.0%; Score 18.2; DB 4; Length 13871;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAA 23
Db 11241 AAGATGCTGAACACAGGAGAGAAA 11263
      |||||
RESULT 24
US-09-949-016-11925/c
; Sequence 11925, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11925
; LENGTH: 143155
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11925

Query Match          65.0%; Score 18.2; DB 4; Length 143155;
Best Local Similarity 87.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAA 23
Db 77034 AATATGCTGAATCGCATAAAAA 77012
      |||||
RESULT 25
US-09-949-016-14368/c
; Sequence 14368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14368
; LENGTH: 143164
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14368

Query Match          65.0%; Score 18.2; DB 4; Length 143164;
Best Local Similarity 87.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 AATATGCTGAACGCGAGAGAAA 23
|||||
Db 77034 AATATGCTGAATGCGATAAAA 77012

RESULT 26

US-09-949-016-14513/c
; Sequence 14513, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14513
; LENGTH: 143173
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14513

Query Match 65.0%; Score 18.2; DB 4; Length 143173;
Best Local Similarity 87.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAA 23
|||||
Db 77043 AATATGCTGAATGCGATAAAA 77021

RESULT 27

US-09-949-016-91405/c
; Sequence 91405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91405
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-91405

Query Match 63.6%; Score 17.8; DB 4; Length 601;
Best Local Similarity 82.6%; Pred. No. 1e+02;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAA 23
|||||
Db 315 AATATGCTGAATGCGATAAAA 293

RESULT 28

US-09-830-433A-31/c
; Sequence 31, Application US/09830433A
; Patent No. 6835384
; GENERAL INFORMATION:
; APPLICANT: AUJAME et al.
; TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
; strains of the Neisseria genus
; FILE REFERENCE: P07180US00/BAS
; CURRENT APPLICATION NUMBER: US/09/830,433A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: FR 98 13 693
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(693)
US-09-830-433A-31

Query Match 62.9%; Score 17.6; DB 4; Length 696;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 210 TGAAGAAACGCGCGGAAACCGCG 187

RESULT 29

US-09-583-110-2433
; Sequence 2433, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2433
; LENGTH: 3351
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2433

Query Match 62.9%; Score 17.6; DB 4; Length 3351;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAAC 24
|||||
Db 830 AATATGCTGAAGCTCTTGAGAAAC 853

RESULT 30

US-09-107-433-999
; Sequence 999, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

```
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
; THERAPEUTICS
;
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 999:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...3363
; SEQUENCE DESCRIPTION: SEQ ID NO: 999:
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; US-09-107-433-999
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; Query Match 62.9%; Score 17.6; DB 4; Length 3363;
; Best Local Similarity 83.3%; Pred. No. 1.8e+02;
; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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; Qy 1 AATATGCTGAACGCGAGAGAAAC 24
; Db 842 AATATGCTGAAGCTCTTGAGAAAC 865
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; RESULT 31
; US-09-270-767-8086
; Sequence 8086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8086
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-8086
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Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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; Qy 1 AATATGCTGAACGCGAGAGAAACCGC 27
; Db 534 AATATGCGAAACGCGCAACAAACCGC 560
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; RESULT 32
; US-09-270-767-23368
; Sequence 23368, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23368
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-23368
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Query Match 62.1%; Score 17.4; DB 4; Length 763;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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; Qy 1 AATATGCTGAACGCGAGAGAAACCGC 27
; Db 534 AATATGCGAAACGCGCAACAAACCGC 560
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; RESULT 33
; US-08-875-233-11
; Sequence 11, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; TITLE OF INVENTION: Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60689
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: WHITE LEAF
FEATURE:
NAME/KEY: CDS
LOCATION: 1..657
PUBLICATION INFORMATION:
AUTHORS: Quemada, H
AUTHORS: Kearney, C
AUTHORS: Gonsalves, D
AUTHORS: Slightom, J
TITLE: Nucleotide Sequences of the Coat Protein
TITLE: Genes and Flanking Regions of Cucumber Mosaic
TITLE: Virus Strains C and WL RNA 3
JOURNAL: J. Gen. Virol.
VOLUME: 70
PAGES: 1065-1073
DATE: 1989
US-08-875-233-11

Query Match 62.1%; Score 17.4; DB 3; Length 983;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACCGGAGAGAAACCGCG 28
DB 113 AGATGCTGAAACTCAATAGAACCTCG 139

RESULT 34
US-09-328-352-1888/c
Sequence 1888, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1888
LENGTH: 1227
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1888

Query Match 62.1%; Score 17.4; DB 4; Length 1227;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGGAGAGAAACCGCG 27
DB 964 AATATGCAAAACCGAAGAAACCGCG 938

RESULT 35
US-09-221-017B-558
Sequence 558, Application US/09221017B
Patent No. 644799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PFI182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PFI546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PE2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NOS: 558:
SEQUENCE CHARACTERISTICS:
LENGTH: 2646 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...2646
US-09-221-017B-558

Query Match 62.1%; Score 17.4; DB 3; Length 2646;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACCGGAGAGAAACCGCG 28
DB 1472 ACAGGATGAAAGCGAAGAAATCCGCG 1498

RESULT 36
US-09-549-872B-3
Sequence 3, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5026
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-549-872B-3

Query Match 62.1%; Score 17.4; DB 4; Length 5026;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AACGCGAGAGAAACCGCG 28
DB 2034 AACGCGAGAGAAACCGCG 2052

RESULT 37

US-09-549-872B-5
; Sequence 5, Application US/09549872B
; Patent No. 6540996

; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard

; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry

; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4

; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596

; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7

; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6612
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-549-872B-5

Query Match 62.1%; Score 17.4; DB 4; Length 6612;
Best Local Similarity 94.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AACGCGAGAGAAACCGCG 28
DB 2646 AACGCGAGAGAAACCGCG 2664

RESULT 38

US-09-549-872B-2
; Sequence 2, Application US/09549872B
; Patent No. 6540996

; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard

; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry

; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4

; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596

; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7

; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11207
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-549-872B-2

Query Match 62.1%; Score 17.4; DB 4; Length 11207;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AACGCGAGAGAAACCGCG 28
DB 2640 AACGCGAGAGAAACCGCG 2658

RESULT 39

US-09-949-016-12428
; Sequence 12428, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12428
; LENGTH: 45225
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12428

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Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGC 27
DB 23730 AGTCTGCTGAAACTGAAGAGAAACCCAC 23756

RESULT 40

US-09-949-016-12428/c
; Sequence 12428, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12428
; LENGTH: 45225

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-085-944-2

Perfect score: 28
Sequence: 1 aatagtgaacgcgagagaaacgcg 28

Scoring table: IDENTITY NUC

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Searched: 7287783 seqs, 3236178273 residues

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Minimum DB seq length: 0

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Maximum Match 100%
Listing first 500 summaries

Database :

Published Applications NA.*

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- 26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	100.0	3381	16	US-10-247-960-2
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4	28	100.0	10649	21	US-10-719-547-14
5	28	100.0	10649	21	US-10-719-547-16
6	28	100.0	10724	19	US-10-699-550-4
7	28	100.0	15159	21	US-10-871-775-30

8	26.4	94.3	10735	19	US-10-699-550-3	Sequence 3, Appli
9	26	92.9	26	9	US-09-840-707A-23	Sequence 23, Appli
10	26	92.9	26	14	US-10-038-557A-23	Sequence 23, Appli
11	24.8	88.6	15053	21	US-10-871-775-32	Sequence 32, Appli
12	22	78.6	72	20	US-10-656-721-26	Sequence 26, Appli
13	19.6	70.0	594	20	US-10-425-115-108018	Sequence 108018,
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15	19	67.9	765	20	US-10-363-345A-20594	Sequence 20594, A
16	19	67.9	765	21	US-10-363-483A-20593	Sequence 20593, A
17	19	67.9	765	21	US-10-363-483A-20594	Sequence 20594, A
18	18.8	67.1	1428	17	US-10-369-493-32952	Sequence 32952, A
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21	18.4	65.7	1443	13	US-10-042-991-11	Sequence 11, Appli
22	18.4	65.7	12305	20	US-10-422-323A-2	Sequence 2, Appli
23	18.4	65.7	12315	20	US-10-422-323A-1	Sequence 1, Appli
24	18.4	65.7	12980	9	US-09-238-076-5	Sequence 5, Appli
25	18.4	65.7	12980	10	US-09-995-937-5	Sequence 5, Appli
26	18.4	65.7	12980	10	US-09-917-563-5	Sequence 5, Appli
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28	18.2	65.0	452	10	US-09-918-995-27460	Sequence 27460, A
29	18.2	65.0	2179	9	US-09-823-245A-434	Sequence 434, App
30	18.2	65.0	3035	22	US-10-887-066-3	Sequence 3, Appli
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32	17.6	62.9	529	18	US-10-424-599-130933	Sequence 130933,
33	17.6	62.9	550	14	US-10-198-846-11819	Sequence 11819, A
34	17.6	62.9	696	21	US-10-909-436-31	Sequence 31, Appli
35	17.6	62.9	838	14	US-10-198-846-3468	Sequence 3468, Ap
36	17.6	62.9	945	17	US-10-398-221-2508	Sequence 2508, Ap
37	17.6	62.9	945	17	US-10-398-221-2571	Sequence 2571, Ap
38	17.6	62.9	966	17	US-10-398-221-553	Sequence 553, App
39	17.6	62.9	966	17	US-10-398-221-554	Sequence 554, App
40	17.6	62.9	1646	17	US-10-282-122A-29374	Sequence 29374, A
41	17.6	62.9	3363	22	US-10-617-320-999	Sequence 999, App
42	17.6	62.9	9718	8	US-08-319-974A-1	Sequence 1, Appli
43	17.6	62.9	684707	17	US-10-398-221-9	Sequence 9, Appli
44	17.6	62.9	684707	17	US-10-398-221-9	Sequence 9, Appli
45	17.6	62.9	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
46	17.4	62.1	341	19	US-10-767-701-19049	Sequence 19049, A
47	17.4	62.1	379	10	US-09-738-269-20	Sequence 20, Appli
48	17.4	62.1	379	13	US-10-023-437-20	Sequence 20, Appli
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53	17.4	62.1	589	20	US-10-363-345A-34197	Sequence 34197, A
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62	17.4	62.1	778	17	US-10-282-122A-36749	Sequence 36749, A
63	17.4	62.1	983	13	US-10-011-033-11	GENERAL INFORMA
64	17.4	62.1	2520	10	US-09-738-269-22	Sequence 22, Appli
65	17.4	62.1	2520	13	US-10-023-437-22	Sequence 22, Appli
66	17.4	62.1	2646	13	US-10-194-163-558	Sequence 558, App
67	17.4	62.1	2784	19	US-10-437-963-21921	Sequence 21921, A
68	17.4	62.1	5026	15	US-10-371-101-3	Sequence 3, Appli
69	17.4	62.1	6612	15	US-10-371-101-5	Sequence 5, Appli
70	17.4	62.1	11207	15	US-10-371-101-2	Sequence 2, Appli
71	17.4	62.1	39726	16	US-10-309-933-1	Sequence 1, Appli
72	17.4	62.1	115780	19	US-10-367-094-96	Sequence 96, Appli
73	17.4	62.1	145068	19	US-10-322-281-33	Sequence 33, Appli
74	17.4	62.1	235070	13	US-10-087-152-1990	Sequence 1990, Ap
75	17.2	61.4	600	22	US-10-972-079-1314	Sequence 1314, Ap
76	17.2	61.4	1428	17	US-10-369-493-33163	Sequence 33163, A
77	17.2	61.4	1506	17	US-10-369-493-41224	Sequence 41224, A
78	17.2	61.4	1689	19	US-10-767-701-15529	Sequence 15529, A
79	17.2	61.4	1960	9	US-09-834-975-833	Sequence 833, App
80	17.2	61.4	1960	20	US-10-357-930-22162	Sequence 22162, A

81	17.2	61.4	1960	20	US-10-357-930-28023	Sequence 28023, A	C 154	16.8	60.0	1654	19	US-10-767-795-6416	Sequence 6416, Ap
82	17.2	61.4	1960	20	US-10-357-930-28979	Sequence 28979, A	155	16.8	60.0	1657	17	US-10-398-221-3320	Sequence 3320, Ap
83	17.2	61.4	3201	19	US-10-664-705-152	Sequence 152, App	C 156	16.8	60.0	1666	18	US-10-424-599-52031	Sequence 52031, A
84	17.2	61.4	3477	19	US-10-437-963-14564	Sequence 14564, A	157	16.8	60.0	2219	18	US-10-425-114-31393	Sequence 31393, A
85	17.2	61.4	3639	16	US-10-437-963-14560	Sequence 14560, A	158	16.8	60.0	2361	17	US-10-282-122A-29289	Sequence 29289, A
86	17.2	61.4	24358	16	US-10-369-978-1	Sequence 1, Appli	159	16.8	60.0	3210	17	US-10-374-780A-1609	Sequence 1609, Ap
87	17.2	61.4	2731748	19	US-10-297-465A-1	Sequence 1, Appli	160	16.8	60.0	3210	18	US-10-412-698B-1658	Sequence 1658, Ap
88	17	60.7	417	9	US-09-770-423-444	Sequence 444, App	C 161	16.8	60.0	3322	18	US-10-437-963-3736	Sequence 3736, Ap
89	17	60.7	437	9	US-09-960-352-2523	Sequence 2523, Ap	162	16.8	60.0	3350	20	US-10-425-115-109187	Sequence 109187, A
90	17	60.7	516	13	US-10-027-632-51441	Sequence 51441, A	C 163	16.8	60.0	3351	19	US-10-437-963-3741	Sequence 3741, Ap
91	17	60.7	516	17	US-10-027-632-51441	Sequence 51441, A	C 164	16.8	60.0	3720	19	US-10-437-963-3735	Sequence 3735, Ap
92	17	60.7	520	13	US-10-027-632-248635	Sequence 248635, A	C 165	16.8	60.0	5064	19	US-10-437-963-85044	Sequence 85044, A
93	17	60.7	520	17	US-10-027-632-248635	Sequence 248635, A	166	16.8	60.0	5064	19	US-09-764-891-8362	Sequence 8362, Ap
94	17	60.7	565	13	US-10-027-632-83075	Sequence 83075, A	167	16.8	60.0	5965	15	US-10-764-891-8362	Sequence 787, App
95	17	60.7	565	13	US-10-027-632-83075	Sequence 83075, A	167	16.8	60.0	5965	15	US-10-425-115-109187	Sequence 5, Appli
96	17	60.7	565	17	US-10-027-632-83075	Sequence 83075, A	168	16.8	60.0	10945	19	US-10-361-002-5	Sequence 5, Appli
97	17	60.7	565	17	US-10-027-632-83075	Sequence 83075, A	169	16.8	60.0	10945	19	US-10-361-004-5	Sequence 5, Appli
98	17	60.7	661	20	US-10-027-632-315971	Sequence 315971, A	170	16.8	60.0	10975	19	US-10-699-550-1	Sequence 1, Appli
99	17	60.7	835	13	US-10-027-632-157206	Sequence 157206, A	171	16.8	60.0	11029	19	US-10-699-550-2	Sequence 2, Appli
100	17	60.7	835	17	US-10-027-632-157206	Sequence 157206, A	172	16.8	60.0	11029	21	US-10-679-520A-66	Sequence 66, Appli
101	17	60.7	14000	21	US-10-893-671-1	Sequence 1, Appli	173	16.8	60.0	11029	21	US-10-706-892-1	Sequence 1, Appli
102	17	60.7	28953	20	US-10-719-993-6811	Sequence 6811, Ap	174	16.8	60.0	11029	22	US-10-706-892-2	Sequence 2, Appli
103	17	60.7	163701	19	US-10-322-281-439	Sequence 439, App	175	16.8	60.0	11029	22	US-10-985-805-1	Sequence 1, Appli
104	17	60.7	227931	17	US-10-085-117-274	Sequence 274, App	C 176	16.8	60.0	12790	21	US-10-893-671-12	Sequence 12, Appli
105	17	60.7	1601042	13	US-10-027-632-59064	Sequence 59064, A	C 177	16.8	60.0	38234	13	US-10-087-192-1762	Sequence 1762, Ap
106	17	60.7	1601042	17	US-10-027-632-59064	Sequence 59064, A	C 178	16.8	60.0	59314	19	US-10-322-281-584	Sequence 584, App
107	16.8	60.0	69	20	US-10-688-489-16	Sequence 16, Appli	C 179	16.6	59.3	188794	21	US-10-322-696-112	Sequence 112, App
108	16.8	60.0	366	20	US-10-425-115-135770	Sequence 135770, A	C 180	16.6	59.3	25	21	US-10-719-900-399987	Sequence 399987, A
109	16.8	60.0	421	20	US-10-425-115-135770	Sequence 135770, A	181	16.6	59.3	34	22	US-10-957-433-56	Sequence 56, Appli
110	16.8	60.0	503	20	US-10-425-115-135770	Sequence 135770, A	182	16.6	59.3	201	20	US-10-425-115-111057	Sequence 111057, A
111	16.8	60.0	503	20	US-10-363-345A-17699	Sequence 17699, A	C 183	16.6	59.3	404	18	US-10-424-599-6683	Sequence 6683, Ap
112	16.8	60.0	503	21	US-10-363-345A-17700	Sequence 17700, A	184	16.6	59.3	409	19	US-10-469-285-701	Sequence 701, App
113	16.8	60.0	503	21	US-10-363-483A-17699	Sequence 17699, A	185	16.6	59.3	447	15	US-10-002-623-531	Sequence 531, App
114	16.8	60.0	503	21	US-10-363-483A-17700	Sequence 17700, A	186	16.6	59.3	487	21	US-10-487-901-6807	Sequence 6807, Ap
115	16.8	60.0	509	20	US-10-363-483A-17235	Sequence 17235, Ap	187	16.6	59.3	504	16	US-10-029-386-7986	Sequence 7986, Ap
116	16.8	60.0	509	20	US-10-363-483A-17236	Sequence 17236, Ap	C 188	16.6	59.3	570	13	US-10-027-632-51307	Sequence 51307, A
117	16.8	60.0	509	21	US-10-363-483A-17235	Sequence 17235, Ap	C 189	16.6	59.3	570	13	US-10-027-632-51308	Sequence 51308, A
118	16.8	60.0	509	21	US-10-363-483A-17236	Sequence 17236, Ap	C 190	16.6	59.3	570	13	US-10-027-632-51309	Sequence 51309, A
119	16.8	60.0	517	20	US-10-425-115-82733	Sequence 82733, A	C 191	16.6	59.3	570	13	US-10-027-632-51310	Sequence 51310, A
120	16.8	60.0	556	18	US-10-424-599-52030	Sequence 52030, A	C 192	16.6	59.3	570	17	US-10-027-632-51307	Sequence 51307, A
121	16.8	60.0	569	18	US-10-424-599-43417	Sequence 43417, A	C 193	16.6	59.3	570	17	US-10-027-632-51308	Sequence 51308, A
122	16.8	60.0	599	22	US-10-972-079-63395	Sequence 63395, A	C 194	16.6	59.3	570	17	US-10-027-632-51309	Sequence 51309, A
123	16.8	60.0	621	9	US-09-764-846-105	Sequence 105, App	C 195	16.6	59.3	575	20	US-10-425-115-76549	Sequence 76549, A
124	16.8	60.0	621	14	US-10-091-483-105	Sequence 105, App	C 196	16.6	59.3	600	22	US-10-972-079-19196	Sequence 19196, A
125	16.8	60.0	634	13	US-10-027-632-6272	Sequence 6272, Ap	C 197	16.6	59.3	680	20	US-10-425-114-8764	Sequence 8764, Ap
126	16.8	60.0	634	17	US-10-027-632-6272	Sequence 6272, Ap	C 198	16.6	59.3	680	20	US-10-425-114-8764	Sequence 8764, Ap
127	16.8	60.0	699	21	US-10-487-901-2868	Sequence 2868, Ap	C 199	16.6	59.3	689	20	US-10-425-115-20769	Sequence 20769, A
128	16.8	60.0	711	18	US-10-424-599-58144	Sequence 58144, A	C 200	16.6	59.3	702	8	US-08-781-986A-314	Sequence 314, App
129	16.8	60.0	716	20	US-10-363-345A-26673	Sequence 26673, A	201	16.6	59.3	702	18	US-10-329-624-314	Sequence 314, App
130	16.8	60.0	716	21	US-10-363-345A-26674	Sequence 26674, A	202	16.6	59.3	707	20	US-10-425-115-20775	Sequence 20775, A
131	16.8	60.0	716	21	US-10-363-345A-26673	Sequence 26673, A	C 203	16.6	59.3	761	20	US-10-425-115-20768	Sequence 20768, A
132	16.8	60.0	725	21	US-10-363-483A-28674	Sequence 28674, A	C 204	16.6	59.3	770	20	US-10-425-115-167404	Sequence 167404, A
133	16.8	60.0	725	17	US-10-027-632-18419	Sequence 18419, A	205	16.6	59.3	804	18	US-10-425-114-15623	Sequence 15623, A
134	16.8	60.0	788	20	US-10-363-345A-7385	Sequence 7385, Ap	206	16.6	59.3	814	13	US-10-027-632-170035	Sequence 170035, A
135	16.8	60.0	788	20	US-10-363-345A-7386	Sequence 7385, Ap	207	16.6	59.3	814	13	US-10-027-632-170036	Sequence 170036, A
136	16.8	60.0	788	21	US-10-363-483A-7385	Sequence 7385, Ap	208	16.6	59.3	814	17	US-10-027-632-170035	Sequence 170035, A
137	16.8	60.0	788	21	US-10-363-483A-7385	Sequence 7385, Ap	209	16.6	59.3	821	21	US-10-472-928-623	Sequence 623, App
138	16.8	60.0	857	21	US-10-363-483A-7386	Sequence 7385, Ap	210	16.6	59.3	831	21	US-10-472-928-1629	Sequence 1629, Ap
139	16.8	60.0	857	20	US-10-363-345A-29811	Sequence 29811, A	211	16.6	59.3	831	21	US-10-472-928-1629	Sequence 1629, Ap
140	16.8	60.0	857	20	US-10-363-345A-29812	Sequence 29812, A	212	16.6	59.3	841	18	US-10-424-599-132044	Sequence 132044, A
141	16.8	60.0	857	21	US-10-363-483A-29811	Sequence 29811, A	213	16.6	59.3	851	8	US-08-961-527-361	Sequence 361, App
142	16.8	60.0	857	21	US-10-363-483A-29812	Sequence 29812, A	214	16.6	59.3	851	17	US-10-158-844-361	Sequence 361, App
143	16.8	60.0	906	17	US-10-282-122A-29547	Sequence 29547, A	215	16.6	59.3	885	18	US-10-425-114-22161	Sequence 22161, A
144	16.8	60.0	996	16	US-10-425-114-34006	Sequence 34006, A	216	16.6	59.3	891	17	US-10-282-122A-35207	Sequence 35207, A
145	16.8	60.0	1058	18	US-10-424-599-73696	Sequence 73696, A	217	16.6	59.3	923	18	US-10-425-114-18889	Sequence 18889, A
146	16.8	60.0	1072	20	US-10-425-115-109185	Sequence 109185, A	218	16.6	59.3	926	20	US-10-425-114-23881	Sequence 23881, A
147	16.8	60.0	1179	20	US-10-363-345A-16665	Sequence 16665, A	C 219	16.6	59.3	968	18	US-10-739-930-850	Sequence 850, App
148	16.8	60.0	1179	21	US-10-363-345A-16666	Sequence 16666, A	220	16.6	59.3	977	20	US-10-425-115-135677	Sequence 135677, A
149	16.8	60.0	1179	21	US-10-363-483A-16665	Sequence 16665, A	221	16.6	59.3	993	18	US-10-425-114-82	Sequence 82, Appli
150	16.8	60.0	1179	21	US-10-363-483A-16666	Sequence 16666, A	222	16.6	59.3	1034	18	US-10-424-599-132042	Sequence 132042, A
151	16.8	60.0	1257	17	US-10-282-122A-9259	Sequence 9259, Ap	223	16.6	59.3	1058	21	US-10-487-901-3076	Sequence 3076, Ap
152	16.8	60.0	1289	17	US-10-369-493-40219	Sequence 40219, A	224	16.6	59.3	1088	21	US-10-487-901-6811	Sequence 6811, Ap
153	16.8	60.0	1382	20	US-10-739-930-446	Sequence 446, App	225	16.6	59.3	1078	20	US-10-425-115-140548	Sequence 140548, A
							226	16.6	59.3	1141	13	US-10-027-632-118252	Sequence 118252, A

227	16.6	59.3	1141	17	US-10-027-632-118252	Sequence 118252,	300	16.4	58.6	675	18	US-10-424-599-84542	Sequence 84542, A
228	16.6	59.3	1191	21	US-10-487-901-4566	Sequence 4566, Ap	301	16.4	58.6	682	9	US-09-770-149-337	Sequence 337, App
229	16.6	59.3	1200	17	US-10-282-122A-8017	Sequence 8017, Ap	c 302	16.4	58.6	742	21	US-10-494-672-345	Sequence 345, App
230	16.6	59.3	1221	20	US-10-363-345A-28151	Sequence 28151, A	303	16.4	58.6	768	9	US-09-777-564-529	Sequence 529, App
231	16.6	59.3	1221	20	US-10-363-345A-28152	Sequence 28152, A	304	16.4	58.6	768	14	US-10-015-219-529	Sequence 529, App
232	16.6	59.3	1221	21	US-10-363-483A-28151	Sequence 28151, A	305	16.4	58.6	849	17	US-10-027-632-9181	Sequence 9181, Ap
233	16.6	59.3	1221	21	US-10-363-483A-28152	Sequence 28152, A	306	16.4	58.6	849	17	US-10-027-632-9181	Sequence 9181, Ap
234	16.6	59.3	1223	20	US-10-363-345A-31157	Sequence 31157, A	c 307	16.4	58.6	988	20	US-10-363-345A-33881	Sequence 33881, A
235	16.6	59.3	1223	20	US-10-363-345A-31158	Sequence 31158, A	308	16.4	58.6	988	20	US-10-363-345A-33882	Sequence 33882, A
236	16.6	59.3	1223	21	US-10-363-483A-31157	Sequence 31157, A	c 309	16.4	58.6	988	21	US-10-363-483A-33881	Sequence 33881, A
237	16.6	59.3	1223	21	US-10-363-483A-31158	Sequence 31158, A	310	16.4	58.6	988	21	US-10-363-483A-33882	Sequence 33882, A
238	16.6	59.3	1399	18	US-10-424-599-25204	Sequence 25204, A	c 311	16.4	58.6	1029	17	US-10-369-493-31372	Sequence 31372, A
239	16.6	59.3	1584	17	US-10-282-122A-11840	Sequence 11840, A	c 312	16.4	58.6	1051	20	US-10-425-115-148939	Sequence 148939, A
240	16.6	59.3	1682	19	US-10-437-963-72027	Sequence 72027, A	c 313	16.4	58.6	1069	20	US-10-425-115-148939	Sequence 148939, A
241	16.6	59.3	1702	19	US-10-369-493-34563	Sequence 34563, A	c 314	16.4	58.6	1137	17	US-10-369-433-28614	Sequence 28614, A
242	16.6	59.3	1974	17	US-10-369-493-40787	Sequence 40787, A	c 315	16.4	58.6	1404	15	US-10-037-270-710	Sequence 710, App
243	16.6	59.3	2000	17	US-10-260-238-2159	Sequence 2159, Ap	c 316	16.4	58.6	1404	17	US-10-117-722-710	Sequence 710, App
244	16.6	59.3	2558	9	US-09-939-980-214	Sequence 214, App	c 317	16.4	58.6	1455	9	US-09-738-626-2886	Sequence 2886, Ap
245	16.6	59.3	2666	9	US-09-853-386-2	Sequence 2, Appli	c 318	16.4	58.6	1568	18	US-10-424-599-58090	Sequence 58090, A
246	16.6	59.3	2666	15	US-10-205-951-44	Sequence 44, Appli	c 319	16.4	58.6	1578	18	US-10-450-055-29	Sequence 29, Appli
247	16.6	59.3	3636	9	US-09-815-242-4234	Sequence 422, Ap	c 320	16.4	58.6	1687	20	US-10-739-930-1658	Sequence 1658, Ap
248	16.6	59.3	4079	18	US-10-424-599-67519	Sequence 67519, A	c 321	16.4	58.6	1687	20	US-10-739-930-1658	Sequence 1658, Ap
249	16.6	59.3	4449	9	US-09-815-242-8386	Sequence 8386, Ap	c 322	16.4	58.6	1790	20	US-10-425-115-49071	Sequence 49071, A
250	16.6	59.3	4594	9	US-09-070-927A-230	Sequence 230, App	c 323	16.4	58.6	1840	19	US-10-437-963-85824	Sequence 85824, A
251	16.6	59.3	9372	16	US-10-293-582-2	Sequence 2, Appli	c 324	16.4	58.6	2354	18	US-10-424-599-125516	Sequence 125516, A
252	16.6	59.3	9372	21	US-10-956-157-1285	Sequence 1285, Ap	c 325	16.4	58.6	2369	9	US-09-895-382-29	Sequence 29, Appli
253	16.6	59.3	25685	21	US-10-292-798-209	Sequence 798, App	c 326	16.4	58.6	2778	19	US-10-437-963-36035	Sequence 36035, A
254	16.6	59.3	134841	13	US-10-087-192-1387	Sequence 1987, Ap	c 327	16.4	58.6	3010	20	US-10-801-847-1	Sequence 1, Appli
255	16.6	59.3	143899	10	US-09-972-546-15	Sequence 15, Appli	c 328	16.4	58.6	3010	20	US-10-801-847-1	Sequence 1, Appli
256	16.6	59.3	143899	19	US-10-735-256-15	Sequence 15, Appli	c 329	16.4	58.6	3050	20	US-10-473-126-151	Sequence 151, App
257	16.6	59.3	152759	21	US-10-322-281-10	Sequence 10, Appli	c 330	16.4	58.6	3128	14	US-10-198-846-9988	Sequence 9988, Ap
258	16.6	59.3	401433	22	US-10-737-088-79	Sequence 79, Appli	c 331	16.4	58.6	3797	20	US-10-425-115-148938	Sequence 148938, A
259	16.6	59.3	401433	22	US-10-737-088-79	Sequence 79, Appli	c 332	16.4	58.6	3797	20	US-10-425-115-148938	Sequence 148938, A
260	16.6	59.3	2162598	21	US-10-472-928-4979	Sequence 4979, Ap	c 333	16.4	58.6	3870	15	US-10-225-567A-143	Sequence 143, App
261	16.6	59.3	2162598	21	US-10-472-928-4979	Sequence 4979, Ap	c 334	16.4	58.6	3870	15	US-10-225-567A-143	Sequence 143, App
262	16.4	58.6	114	9	US-09-969-373-1446	Sequence 1446, Ap	c 335	16.4	58.6	5856	17	US-10-191-997-100	Sequence 100, App
263	16.4	58.6	173	19	US-10-437-963-27336	Sequence 27336, A	c 336	16.4	58.6	5856	17	US-10-191-997-100	Sequence 100, App
264	16.4	58.6	214	10	US-09-880-107-1805	Sequence 1805, Ap	c 337	16.4	58.6	6050	15	US-10-311-455-852	Sequence 852, App
265	16.4	58.6	214	10	US-09-960-706-535	Sequence 535, App	c 338	16.4	58.6	6050	15	US-10-172-086-49	Sequence 49, Appli
266	16.4	58.6	329	16	US-09-873-319-329	Sequence 329, App	c 339	16.4	58.6	6050	19	US-10-311-507-19	Sequence 19, App
267	16.4	58.6	316	17	US-10-369-493-30337	Sequence 30337, A	c 340	16.4	58.6	6050	20	US-10-480-846-49	Sequence 49, Appli
268	16.4	58.6	380	20	US-10-425-115-120741	Sequence 120741, A	c 341	16.4	58.6	6235	15	US-10-311-455-759	Sequence 759, App
269	16.4	58.6	390	9	US-09-738-626-692	Sequence 692, App	c 342	16.4	58.6	6235	15	US-10-311-455-759	Sequence 759, App
270	16.4	58.6	475	10	US-09-764-891-1741	Sequence 1741, Ap	c 343	16.4	58.6	7309	18	US-10-221-714A-289	Sequence 289, App
271	16.4	58.6	504	20	US-10-363-345A-17145	Sequence 17145, A	c 344	16.4	58.6	7309	18	US-10-221-714A-289	Sequence 289, App
272	16.4	58.6	504	20	US-10-363-345A-17146	Sequence 17146, A	c 345	16.4	58.6	7309	18	US-10-221-714A-289	Sequence 289, App
273	16.4	58.6	504	21	US-10-363-483A-17145	Sequence 17145, A	c 346	16.4	58.6	13606	14	US-10-239-676-166	Sequence 166, App
274	16.4	58.6	504	21	US-10-363-483A-17146	Sequence 17146, A	c 347	16.4	58.6	13606	15	US-10-311-455-1784	Sequence 1784, Ap
275	16.4	58.6	599	22	US-10-972-079-73120	Sequence 73120, A	c 348	16.4	58.6	13606	15	US-10-240-453-188	Sequence 188, App
276	16.4	58.6	600	22	US-10-972-079-84546	Sequence 84546, A	c 349	16.4	58.6	13606	15	US-10-240-453-188	Sequence 188, App
277	16.4	58.6	600	22	US-10-972-079-84547	Sequence 84547, A	c 350	16.4	58.6	55889	19	US-10-741-601-5684	Sequence 5684, Ap
278	16.4	58.6	600	22	US-10-972-079-84548	Sequence 84548, A	c 351	16.4	58.6	55889	21	US-10-741-601-5684	Sequence 5684, Ap
279	16.4	58.6	605	13	US-10-027-632-191203	Sequence 191203, A	c 352	16.4	58.6	106608	20	US-10-417-600-17734	Sequence 17734, A
280	16.4	58.6	605	13	US-10-027-632-191204	Sequence 191204, A	c 353	16.4	58.6	106608	20	US-10-417-600-17734	Sequence 17734, A
281	16.4	58.6	605	13	US-10-027-632-191205	Sequence 191205, A	c 354	16.4	58.6	175590	10	US-09-911-077A-13	Sequence 13, Appli
282	16.4	58.6	605	17	US-10-027-632-191203	Sequence 191203, A	c 355	16.4	58.6	175590	10	US-09-911-077A-13	Sequence 13, Appli
283	16.4	58.6	605	17	US-10-027-632-191204	Sequence 191204, A	c 356	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
284	16.4	58.6	605	17	US-10-027-632-191205	Sequence 191205, A	c 357	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
285	16.4	58.6	612	9	US-09-738-626-2995	Sequence 2995, Ap	c 358	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
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287	16.4	58.6	614	20	US-10-363-345A-37293	Sequence 37293, A	c 360	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
288	16.4	58.6	614	21	US-10-363-345A-37294	Sequence 37294, A	c 361	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
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290	16.4	58.6	621	17	US-10-369-493-32728	Sequence 32728, A	c 363	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
291	16.4	58.6	630	9	US-09-777-564-1701	Sequence 1701, Ap	c 364	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
292	16.4	58.6	630	14	US-10-015-219-1701	Sequence 1701, Ap	c 365	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
293	16.4	58.6	631	13	US-10-282-122A-25343	Sequence 25343, A	c 366	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
294	16.4	58.6	652	13	US-10-194-163-105	Sequence 105, App	c 367	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
295	16.4	58.6	652	13	US-10-194-163-105	Sequence 105, App	c 368	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
296	16.4	58.6	657	20	US-10-363-345A-18311	Sequence 18311, A	c 369	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
297	16.4	58.6	657	20	US-10-363-345A-18312	Sequence 18312, A	c 370	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
298	16.4	58.6	657	21	US-10-363-483A-18311	Sequence 18311, A	c 371	16.4	58.6	175590	10	US-10-724-806-13	Sequence 13, Appli
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373	16.2	57.9	493	9	US-09-895-793-450	Sequence 450, App	446	21	21	US-10-913-996-8	Sequence 8, Appli
374	16.2	57.9	493	9	US-09-895-814-450	Sequence 450, App	447	21	21	US-10-913-996-9	Sequence 9, Appli
375	16.2	57.9	493	13	US-10-012-896-450	Sequence 450, App	c 448	210	210	US-10-913-996-16	Sequence 19, Appl
376	16.2	57.9	493	14	US-10-010-940-450	Sequence 450, App	449	210	9	US-09-728-444-159	Sequence 56, Appl
377	16.2	57.9	493	16	US-10-144-678A-450	Sequence 450, App	450	214	9	US-09-728-446-1394	Sequence 1394, Ap
378	16.2	57.9	493	16	US-10-294-025-450	Sequence 450, App	c 451	267	19	US-10-437-963-5460	Sequence 5460, Ap
379	16.2	57.9	525	9	US-09-398-598-440	Sequence 440, App	452	267	19	US-10-437-963-86035	Sequence 86035, A
380	16.2	57.9	537	9	US-09-796-692-8874	Sequence 8874, Ap	453	277	9	US-09-728-446-1393	Sequence 1393, Ap
381	16.2	57.9	537	14	US-10-040-863-8874	Sequence 8874, Ap	454	296	14	US-10-060-036-3038	Sequence 3038, Ap
382	16.2	57.9	537	17	US-10-057-475B-8874	Sequence 8874, Ap	455	365	20	US-10-425-115-85477	Sequence 85477, A
383	16.2	57.9	537	17	US-10-154-884B-8874	Sequence 8874, Ap	456	395	10	US-09-803-719-1367	Sequence 1367, Ap
384	16.2	57.9	537	17	US-10-764-324-8874	Sequence 8874, Ap	c 457	398	19	US-10-674-124A-23252	Sequence 23252, A
c 385	16.2	57.9	538	16	US-10-029-386-5119	Sequence 5119, Ap	458	431	18	US-10-424-599-47255	Sequence 47255, A
386	16.2	57.9	559	9	US-09-998-598-521	Sequence 521, App	c 459	446	20	US-10-425-115-17555	Sequence 17555, A
387	16.2	57.9	581	9	US-09-796-692-7189	Sequence 7189, Ap	460	474	18	US-10-424-599-54281	Sequence 54281, A
388	16.2	57.9	581	14	US-10-040-863-7189	Sequence 7189, Ap	461	524	17	US-10-369-493-30113	Sequence 30113, A
389	16.2	57.9	581	17	US-10-057-475B-7189	Sequence 7189, Ap	462	534	19	US-10-021-323-16750	Sequence 16750, A
390	16.2	57.9	581	17	US-10-154-884B-7189	Sequence 7189, Ap	463	538	20	US-10-425-115-133165	Sequence 133165, A
391	16.2	57.9	581	19	US-10-764-324-7189	Sequence 7189, Ap	464	541	20	US-10-425-115-104069	Sequence 104069, A
c 392	16.2	57.9	597	19	US-10-437-963-37273	Sequence 37273, A	465	573	13	US-10-027-632-268636	Sequence 268636, A
393	16.2	57.9	600	21	US-10-956-157-7369	Sequence 7369, Ap	466	573	13	US-10-027-632-268637	Sequence 268637, A
c 394	16.2	57.9	616	13	US-10-027-632-235893	Sequence 235893, A	467	573	17	US-10-027-632-268637	Sequence 268637, A
c 395	16.2	57.9	623	9	US-10-027-632-235893	Sequence 235893, A	468	584	9	US-09-864-761-14937	Sequence 14937, A
396	16.2	57.9	623	9	US-09-998-598-2387	Sequence 2387, Ap	c 469	590	18	US-10-424-599-906	Sequence 906, App
397	16.2	57.9	644	20	US-10-653-047-5466	Sequence 5466, Ap	c 470	598	13	US-10-027-632-133185	Sequence 133185, A
398	16.2	57.9	657	10	US-09-814-353-5650	Sequence 5650, Ap	c 472	598	17	US-10-027-632-133185	Sequence 133185, A
399	16.2	57.9	657	10	US-09-814-353-11936	Sequence 11936, A	473	600	22	US-10-972-079-85001	Sequence 85001, A
c 400	16.2	57.9	730	9	US-09-879-536-693	Sequence 693, App	c 474	613	18	US-10-424-599-52907	Sequence 52907, A
c 401	16.2	57.9	885	21	US-10-282-122A-40988	Sequence 40988, A	475	615	13	US-10-027-632-259025	Sequence 259025, A
c 402	16.2	57.9	885	17	US-10-956-157-2134	Sequence 2134, Ap	476	615	13	US-10-027-632-259026	Sequence 259026, A
c 403	16.2	57.9	984	17	US-10-282-122A-39413	Sequence 39413, A	477	615	13	US-10-027-632-259027	Sequence 259027, A
c 404	16.2	57.9	989	17	US-10-282-122A-36705	Sequence 36705, A	478	615	13	US-10-027-632-259025	Sequence 259025, A
c 405	16.2	57.9	1112	20	US-10-363-345A-29477	Sequence 29477, A	479	615	17	US-10-027-632-259026	Sequence 259026, A
c 406	16.2	57.9	1112	20	US-10-363-345A-29478	Sequence 29478, A	480	615	17	US-10-027-632-259027	Sequence 259027, A
c 407	16.2	57.9	1112	21	US-10-363-483A-29477	Sequence 29477, A	c 481	622	18	US-10-424-599-52890	Sequence 52890, A
c 408	16.2	57.9	1194	21	US-09-814-353-21719	Sequence 21719, A	c 482	637	13	US-10-027-632-236067	Sequence 236067, A
c 409	16.2	57.9	1194	21	US-09-814-353-21719	Sequence 21719, A	c 483	637	13	US-10-027-632-236067	Sequence 236067, A
c 410	16.2	57.9	1299	9	US-09-938-842A-2347	Sequence 2347, Ap	c 484	640	13	US-10-027-632-278091	Sequence 278091, A
c 411	16.2	57.9	1299	11	US-09-938-842A-2347	Sequence 2347, Ap	c 485	640	13	US-10-027-632-278091	Sequence 278091, A
c 412	16.2	57.9	1304	19	US-10-473-576-43	Sequence 43, Appl	c 487	640	17	US-10-027-632-278092	Sequence 278092, A
c 413	16.2	57.9	1308	10	US-09-764-891-7057	Sequence 7057, App	c 488	648	9	US-09-815-242-7367	Sequence 7367, Ap
c 414	16.2	57.9	1643	17	US-10-094-749-515	Sequence 7057, App	489	648	17	US-10-282-122A-22853	Sequence 22853, A
c 415	16.2	57.9	1847	13	US-10-027-632-97793	Sequence 97793, A	490	654	19	US-10-767-701-25981	Sequence 25981, A
c 416	16.2	57.9	1847	13	US-10-027-632-97794	Sequence 97794, A	491	654	19	US-10-767-701-25981	Sequence 25981, A
c 417	16.2	57.9	1847	13	US-10-027-632-98948	Sequence 98948, A	c 492	663	13	US-10-027-632-24761	Sequence 24761, A
c 418	16.2	57.9	1847	13	US-10-027-632-98948	Sequence 98948, A	c 493	663	17	US-10-027-632-24761	Sequence 24761, A
c 419	16.2	57.9	1847	13	US-10-027-632-98948	Sequence 98948, A	c 494	663	17	US-10-369-493-41345	Sequence 41345, A
c 420	16.2	57.9	1847	17	US-10-027-632-97794	Sequence 97794, A	c 495	674	20	US-10-653-047-6875	Sequence 6875, Ap
c 421	16.2	57.9	1847	17	US-10-027-632-97794	Sequence 97794, A	c 496	674	20	US-10-653-047-6875	Sequence 6875, Ap
c 422	16.2	57.9	1847	17	US-10-027-632-98949	Sequence 98949, A	c 497	690	18	US-10-660-811A-35	Sequence 35, Appl
c 423	16.2	57.9	1880	21	US-10-956-157-4586	Sequence 4586, Ap	c 498	690	18	US-10-335-977-2076	Sequence 2076, Ap
c 424	16.2	57.9	2000	17	US-10-260-238-1978	Sequence 1978, Ap	c 499	696	21	US-10-910-943-270	Sequence 270, App
c 425	16.2	57.9	2715	17	US-10-369-493-27260	Sequence 27260, A	c 500	696	21	US-10-909-436-70	Sequence 70, Appl
c 426	16.2	57.9	3635	18	US-10-112-944-29	Sequence 29, Appl		700	19	US-10-767-701-1368	Sequence 1268, Ap
c 427	16.2	57.9	3747	17	US-10-399-214-17	Sequence 17, Appl		700	19	US-10-767-701-1368	Sequence 236, App
c 428	16.2	57.9	3747	20	US-10-482-952-17	Sequence 17, Appl					
c 429	16.2	57.9	4598	10	US-09-822-846-118	Sequence 118, App					
c 430	16.2	57.9	4616	18	US-10-112-944-28	Sequence 28, Appl					
c 431	16.2	57.9	7042	9	US-09-876-667-1	Sequence 1, Appl					
c 432	16.2	57.9	7042	15	US-10-171-581-264	Sequence 264, App					
c 433	16.2	57.9	7042	16	US-10-141-618-9	Sequence 9, Appli					
c 434	16.2	57.9	7042	17	US-10-441-281-24	Sequence 24, Appl					
c 435	16.2	57.9	7042	17	US-10-399-214-21	Sequence 21, Appl					
c 436	16.2	57.9	7042	21	US-10-764-503-24	Sequence 24, Appl					
c 437	16.2	57.9	7042	21	US-10-956-157-568	Sequence 568, App					
c 438	16.2	57.9	7075	9	US-09-876-667-15	Sequence 15, Appl					
c 439	16.2	57.9	96596	18	US-10-052-482-10	Sequence 10, Appl					
c 440	16.2	57.9	138837	19	US-10-322-281-146	Sequence 146, App					
c 441	16.2	57.9	256525	13	US-10-087-192-451	Sequence 451, App					
c 442	16.2	57.9	397658	9	US-09-813-320-3	Sequence 3, Appli					
c 443	16.2	57.9	397658	24	US-11-044-879-3	Sequence 3, Appli					
c 444	16.2	57.1	20	21	US-10-913-996-6	Sequence 6, Appli					
c 445	16.2	57.1	20	21	US-10-913-996-17	Sequence 17, Appl					

ALIGNMENTS

RESULT 1
US-10-085-944-2
; Sequence 2, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2


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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-085-944-2

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RESULT 2
US-10-247-960-2
; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Coller, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

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RESULT 3
US-10-719-547-18
; Sequence 18, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; TITLE OF INVENTION: ATTENUATING DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/719,547
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Dengue 4 virus strain 2A
US-10-719-547-14

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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
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RESULT 4
US-10-719-547-14
; Sequence 14, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; TITLE OF INVENTION: ATTENUATING DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Dengue 4 virus strain 2A
US-10-719-547-14

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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
    |||||

RESULT 5
US-10-719-547-16
; Sequence 16, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; TITLE OF INVENTION: ATTENUATING DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
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; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Recombinant Dengue 4 virus strain rDEN4
US-10-719-547-16

Query Match      100.0%; Score 28; DB 21; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 138 AATATGCTGAAACCGGAGAGAAACCGCG 165

RESULT 6
US-10-699-550-4
; Sequence 4, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10724
; TYPE: DNA
; ORGANISM: Dengue virus type 2
US-10-699-550-4

Query Match      100.0%; Score 28; DB 19; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 136 AATATGCTGAAACCGGAGAGAAACCGCG 163

RESULT 7
US-10-871-775-30
; Sequence 30, Application US/10871775
; Publication No. US20050100886A1
; GENERAL INFORMATION:
; APPLICANT: Pletnev, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; TITLE OF INVENTION: PREVENT DISEASE CAUSED BY WEST NILE VIRUS.
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775

; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Recombinant Dengue 4 virus strain rDEN4
US-10-719-547-16

Query Match      100.0%; Score 28; DB 21; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 138 AATATGCTGAAACCGGAGAGAAACCGCG 165

RESULT 6
US-10-699-550-4
; Sequence 4, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10724
; TYPE: DNA
; ORGANISM: Dengue virus type 2
US-10-699-550-4

Query Match      100.0%; Score 28; DB 19; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 136 AATATGCTGAAACCGGAGAGAAACCGCG 163

RESULT 7
US-10-871-775-30
; Sequence 30, Application US/10871775
; Publication No. US20050100886A1
; GENERAL INFORMATION:
; APPLICANT: Pletnev, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; TITLE OF INVENTION: PREVENT DISEASE CAUSED BY WEST NILE VIRUS.
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775

; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US03/00594
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,281
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dengue2 (Tonga/74) plaemid p2
US-10-871-775-30

Query Match      100.0%; Score 28; DB 21; Length 15159;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 136 AATATGCTGAAACCGGAGAGAAACCGCG 163

RESULT 8
US-10-699-550-3
; Sequence 3, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10735
; TYPE: DNA
; ORGANISM: Dengue virus type 1
US-10-699-550-3

Query Match      94.3%; Score 26.4; DB 19; Length 10735;
Best Local Similarity 96.4%; Pred. No. 0.092;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 134 AATATGCTGAAACCGGAGAGAAACCGCG 161

RESULT 9
US-09-840-707A-23
; Sequence 23, Application US/09840707A
; Patent No. US20020077276A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
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; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-09-840-707A-23

Query Match          92.9%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCG 26
   |||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 10
US-10-038-557A-23
; Sequence 23, Application US/10038557A
; Publication No. US20030092684A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301D
; CURRENT APPLICATION NUMBER: US/10/038,557A
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/840,707
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-10-038-557A-23

Query Match          92.9%; Score 26; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCG 26
   |||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 11
US-10-871-775-32
; Sequence 32, Application US/10871775
; Publication No. US20050100886A1
; GENERAL INFORMATION:
; APPLICANT: Pletnev, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
```

```
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; TITLE OF INVENTION: PREVENT DISEASE CAUSED BY WEST NILE VIRUS.
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US03/00594
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,281
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 15053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dengue 3 (sleman/78) plasmid p3
US-10-871-775-32

Query Match          88.6%; Score 24.8; DB 21; Length 15053;
Best Local Similarity 92.9%; Pred. No. 0.5;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
   |||||
Db 134 AATATGCTGAAACGCGTGAGAAACCGTG 161

RESULT 12
US-10-656-721-26
; Sequence 26, Application US/10656721
; Publication No. US20040265338A1
; GENERAL INFORMATION:
; APPLICANT: Pang, Xiaowu
; APPLICANT: Dayton, Andrew I.
; APPLICANT: Zhang, Minglie
; TITLE OF INVENTION: SURGENOMIC REPLICONS OF THE FLAVIVIRUS
; TITLE OF INVENTION: DENGUE
; FILE REFERENCE: NIH202.001C1
; CURRENT APPLICATION NUMBER: US/10/656,721
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/US02/06962
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/274,684
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' primer
US-10-656-721-26

Query Match          78.6%; Score 22; DB 20; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAA 22
   |||||
Db 28 AATATGCTGAAACGCGAGAGAA 49

RESULT 13
US-10-425-115-108018
; Sequence 108018, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
```

```
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 108018
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; APPLICANT: Kurt Berlin
; OTHER INFORMATION: Clone ID: MRT4577_30008C.1
; US-10-425-115-108018

Query Match          70.0%; Score 19.6; DB 20; Length 594;
Best Local Similarity 84.6%; Pred. No. 75;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACCGC 27
    |||||
DB 552 ATATGCTGATTACGAGAGAAACAGC 577

RESULT 14
US-10-363-345A-20593/c
; Sequence 20593, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20593
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20593
US-10-363-345A-20593

Query Match          67.9%; Score 19; DB 20; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACCGC 28
    |||||
DB 325 ATACGCCGAAACGCGAGAGAAACCGC 299

RESULT 15
US-10-363-345A-20594
; Sequence 20594, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
```

```
; SEQ ID NO 20594
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20594
US-10-363-345A-20594

Query Match          67.9%; Score 19; DB 20; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACCGC 28
    |||||
DB 441 ATACGCCGAAACGCGAGAGAAACCGC 467

RESULT 16
US-10-363-483A-20593/c
; Sequence 20593, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20593
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20593
US-10-363-483A-20593

Query Match          67.9%; Score 19; DB 21; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACCGC 28
    |||||
DB 325 ATACGCCGAAACGCGAGAGAAACCGC 299

RESULT 17
US-10-363-483A-20594
; Sequence 20594, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20594
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20594
US-10-363-483A-20594
```

Query Match 67.9%; Score 19; DB 21; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 441 ATACGCGGAAACGGAGAAACCGCG 467

RESULT 18
US-10-369-493-32952/c
; Sequence 32952, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32952
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-369-493-32952

Query Match 67.1%; Score 18.8; DB 17; Length 1428;
Best Local Similarity 90.3%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAAACGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 1184 CGGAACGGAGAGAAACCGCG 1163

RESULT 19
US-10-156-761-2286
; Sequence 2286, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2286
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1602)
US-10-156-761-2286

Query Match 66.4%; Score 18.6; DB 15; Length 1602;

Query Match 67.9%; Score 19; DB 21; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 441 ATACGCGGAAACGGAGAAACCGCG 467

RESULT 18
US-10-369-493-32952/c
; Sequence 32952, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32952
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-369-493-32952

Query Match 67.1%; Score 18.8; DB 17; Length 1428;
Best Local Similarity 90.3%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAAACGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 1184 CGGAACGGAGAGAAACCGCG 1163

RESULT 19
US-10-156-761-2286
; Sequence 2286, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2286
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1602)
US-10-156-761-2286

Query Match 66.4%; Score 18.6; DB 15; Length 1602;

Best Local Similarity 84.0%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGAAACGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 115 AAGTGCACCGCGAGAGCAACCGCG 139

RESULT 20
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 66.4%; Score 18.6; DB 15; Length 9025608;
Best Local Similarity 84.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGAAACGGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 2778649 AAGTGCACCGCGAGAGCAACCGCG 2778625

RESULT 21
US-10-042-991-11
; Sequence 11, Application US/10042991
; Publication No. US20020142407A1
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIMUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.000103
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match 65.7%; Score 18.4; DB 13; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.9e+02;


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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/995,937
  FILING DATE: 28-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/034,756
  FILING DATE: 04-May-1998
ATTORNEY/AGENT INFORMATION:
  NAME: HOLLAND, DONALD R.
  REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 314-727-5188
  TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 12980 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-995-937-5

Query Match      65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AATATGCTGAAACCGGAGAGAAACCGCG 28
Db      9714 AATATGCTAAACCGCGCATACCCCGCG 9687

RESULT 26
US-09-917-563-5/c
Sequence 5, Application US/09917563
Publication No. US20030073080A1
GENERAL INFORMATION:
  APPLICANT: RICE, CHARLES et al.
  TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
  ADDRESSEE: HOWELL & HAFERKAMP, L.C.
  STREET: 7733 FORSYTH BLVD., SUITE 1400
  CITY: ST. LOUIS
  STATE: MO
  COUNTRY: USA
  ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/917,563
  FILING DATE: 27-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/238,076
  FILING DATE: 26-JAN-1999
ATTORNEY/AGENT INFORMATION:
  NAME: HOLLAND, DONALD R.
  REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 12980 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-917-563-5

Query Match      65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AATATGCTGAAACCGGAGAGAAACCGCG 28
Db      9714 AATATGCTAAACCGCGCATACCCCGCG 9687

RESULT 27
US-10-719-900-399988/c
Sequence 399988, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
  APPLICANT: Xue Mei Zhou
  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
  FILE REFERENCE: 3528.1
  CURRENT APPLICATION NUMBER: US/10/719,900
  CURRENT FILING DATE: 2003-11-20
  PRIOR APPLICATION NUMBER: 60/427,808
  PRIOR FILING DATE: 2002-11-20
  NUMBER OF SEQ ID NOS: 982914
  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
  SEQ ID NO 399988
  LENGTH: 25
  TYPE: DNA
  ORGANISM: Mus musculus
US-10-719-900-399988

Query Match      65.0%; Score 18.2; DB 21; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AATATGCTGAAACCGGAGAGAAA 23
Db      24 AATTTGCTGAAACCGGAGAGAAA 2

RESULT 28
US-09-918-995-27460
Sequence 27460, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
  APPLICANT: Hyseq, Inc.
  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
  TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
  FILE REFERENCE: 20411-756
  CURRENT APPLICATION NUMBER: US/09/918,995
  CURRENT FILING DATE: 2001-07-30
  PRIOR APPLICATION NUMBER: US/09/235,076
  PRIOR FILING DATE: 1999-01-20
  NUMBER OF SEQ ID NOS: 38054
  SOFTWARE: FastSeq for Windows Version 3.0
  SEQ ID NO 27460
  LENGTH: 452
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc_feature
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RESULT 33


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US-10-198-846-11819/c
; Sequence 11819, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11819
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 506, 549, 550
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11819
Query Match 62.9%; Score 17.6; DB 14; Length 550;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAAC 24
Db 45 AATTTCGGAACACTGGAGAGAAAC 22
RESULT 34
US-10-909-436-31/c
; Sequence 31, Application US/10909436
; Publication No. US20050032103A1
; GENERAL INFORMATION:
; APPLICANT: AUJME et al.
; TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
; TITLE OF INVENTION: strains of the Neisseria genus
; FILE REFERENCE: P07180US00/BAS
; CURRENT APPLICATION NUMBER: US/10/909,436
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: FR 98 13 693
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; NAME/KEY: CDS
; LOCATION: (1)...(693)
US-10-909-436-31
Query Match 62.9%; Score 17.6; DB 21; Length 696;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 TGCTGAAACGCGAGAGAAACCGG 28
Db 210 TGAAGAAACGCGGCGGAAACCGG 187
RESULT 35
US-10-198-846-3468/c
; Sequence 3468, Application US/10198846
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```
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3468
; LENGTH: 838
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 557, 616, 641, 691, 749, 765, 796, 798, 815, 821
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-3468
Query Match 62.9%; Score 17.6; DB 14; Length 838;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAAC 24
Db 108 AATTTCGGAACACTGGAGAGAAAC 85
RESULT 36
US-10-398-221-2508
; Sequence 2508, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2508
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2508
Query Match 62.9%; Score 17.6; DB 17; Length 945;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 TATGCTGAAACGCGAGAGAAACCG 26
Db 193 TATGCTGAAACACATGAGAGAAACAG 216
RESULT 37
US-10-398-221-2571
; Sequence 2571, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
```

```
/ APPLICANT: GLASER, Philippe
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 - US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ CURRENT FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: FR 00/12 697
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2571
/ LENGTH: 945
/ TYPE: DNA
/ ORGANISM: Listeria innocua
US-10-398-221-5571

Query Match      62.9%; Score 17.6; DB 17; Length 945;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCG 26
   |||||
Db 193 TATGCTGAACACATGAGAAACAG 216
   |||||

RESULT 38
US-10-398-221-553
/ Sequence 553, Application US/10398221
/ Publication No. US20040018514A1
/ GENERAL INFORMATION:
/ APPLICANT: KUNST, Frederik
/ APPLICANT: GLASER, Philippe
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 - US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ CURRENT FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: FR 00/12 697
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 553
/ LENGTH: 966
/ TYPE: DNA
/ ORGANISM: Listeria innocua
US-10-398-221-553

Query Match      62.9%; Score 17.6; DB 17; Length 966;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCG 26
   |||||
Db 214 TATGCTGAACACATGAGAAACAG 237
   |||||

RESULT 39
US-10-398-221-554
/ Sequence 554, Application US/10398221
/ Publication No. US20040018514A1
/ GENERAL INFORMATION:
/ APPLICANT: KUNST, Frederik
/ APPLICANT: GLASER, Philippe
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 - US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ CURRENT FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: FR 00/12 697
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 554
/ LENGTH: 966
/ TYPE: DNA
/ ORGANISM: Listeria innocua
US-10-398-221-554

Query Match      62.9%; Score 17.6; DB 17; Length 966;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCG 26
   |||||
Db 214 TATGCTGAACACATGAGAAACAG 237
   |||||

RESULT 40
US-10-282-122A-29374/C
/ Sequence 29374, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 29374
/ LENGTH: 1646
/ TYPE: DNA
/ ORGANISM: Neisseria meningitidis
US-10-282-122A-29374

Query Match      62.9%; Score 17.6; DB 17; Length 1646;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGCTGAACGCGAGAGAAACCG 28
   || ||||| ||||| ||||| |||||
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Db 210 TGAAGAAACGGCGGGAAACCGCG 187

Search completed: July 31, 2005, 15:46:25
Job time : 367.5 secs

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